

Qy 61 FVKIMKORGINVVVELTDINVAETVDLASKAAKEEF1ETFTFLEETVPVLTEANKKAVRAFLLS 120

Db 61 FVAELKANDINNVVELIDLVAETDYLASQEAOKDLIEBLEDSEPVLSSEHKVVVRNFLKA 120
QY 121 KPT-HEMVFEFMSGITYKVELGVSENELIVDPMPNLVFTTRDPFASVGVNGVTIHPMYRIVR 179
Db 121 KKTSRKLVINMAGITKYDLGIEADHLLVDPMPNLVFTTRDPFASVGVNGVTIHPMYRKYVR 180
QY 180 RRETFLARFVRNHPKLVKTPWYDDPAKMPVIEGGDVFIYNNETLVVGVSERTDLDITTL 239
Db 181 QRETLPSRFVPSNHPKLVNTWYDDPSLKLSIEGDDVFIYNNETLVVGVSERTDLDITTL 240
QY 240 LAKNIKANKVEFKRIIVAINVPKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNIVANKCEFKRIIVAINVPKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPOPQNLGLPLDKLLASIIINKEPVLIPDGAGATEMEIARETFTDGTNYLAIKPG 359
Db 301 NGGAEPOPQNLGLPLDKLLASIIINKEPVLIPDGAGATEMEIARETFTDGTNYLAIKPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVKW 409
Db 361 VIGYSRNEKTNAALEAGIKVLPFHGNQSLGGMGNARCMSPLSRKDVVKW 410

RESULT 2
S68515
A:Title: probable arginine deiminase (EC 3.5.3.6) - Mycoplasma arginini (fragment)
C:Species: Mycoplasma arginini
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 07-Dec-1999
C:Accession: S68515; S68514
R:Wilms, M.; Shevchenko, A.; Houthaave, T.; Breit, S.; Schweigerer, L.; Fotsis, T.; Mann, Nature 379, 466-469, 1996
A:Title: Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray
A:Reference number: S68514; MUID:96158883; PMID:8559255
A:Accession: S68515
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-410 <WIL>
A:Cross-references: EMBL:X93471
A:Note: only a part of the translation is shown
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
A:Accession: S68514
A:Molecule type: protein
A:Residues: 103-105,'X',107-111;126,'XX',129-134,'X',136-137;161-167,'D',169-171,'X',173
A:Note: peptides obtained by mass spectrometry
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: arginine deiminase arca
C:Keywords: hydrolase

Query Match 80.3%; Score 1702.5; DB 2; Length 410;
Best Local Similarity 78.3%; Pred. No. 4.6e-113;
Matches 321; Conservative 48; Mismatches 40; Indels 1; Gaps 1;
QY 1 MSVPDSKFNHGVYSEIGELETVLVHPGREGIDYITPARLDELFSAILSHDARKEHQ 60
Db 1 MSVPDSKFNHGVYSEIGDLESVLVHPGREGIDYITPARLDELFSAILSHDARKEHQ 60
QY 61 FVKIMKORGINVELTDLVAETDYLASKAAKEFIETFLBETVPLTEANKKAVRAPL 120
Db 61 FVEILKKQGINVELVLDVWETYNLVKTKQELKDLFODSEPVLSPEHRKAVKEFL 120
QY 121 -KPTHEMVFEFMSGITYKVELGVSENELIVDPMPNLVFTTRDPFASVGVNGVTIHPMYRIVR 179
Db 121 LKSTKELIQVMAGITKYDLGIEADHLLVDPMPNLVFTTRDPFASVGVNGVTIHPMYRKYVR 180
QY 180 RRETFLARFVRNHPKLVKTPWYDDPAKMPVIEGGDVFIYNNETLVVGVSERTDLDITTL 239
Db 181 QRETLPSRFVPSNHPKLVNTWYDDPSLKLSIEGDDVFIYNNETLVVGVSERTDLDITTL 240
QY 240 LAKNIKANKVEFKRIIVAINVPKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNIKANKCEFKRIIVAINVPKWTNLMHLDITWLTMDKNKFLYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPOPQNLGLPLDKLLASIIINKEPVLIPDGAGATEMEIARETFTDGTNYLAIKPG 359
Db 301 NGGAEPOPQNLGLPLDKLLASIIINKEPVLIPDGAGATEMEIARETFTDGTNYLAIKPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDVVKW 409
Db 361 VIGYSRNEKTNAALEAGIKVLPFHGNQSLGGMGNARCMSPLSRKDVVKW 410

RESULT 3
A38835
streptococcal antitumor protein - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A38835; A33225; S16694
R:Kanaoka, M.; Kawanaka, C.; Negoro, T.; Fukita, Y.; Taya, K.; Agui, H. Agric. Biol. Chem. 51, 2641-2648, 1987
A:Title: Cloning and expression of the antitumor glycoprotein gene of Streptococcus pyogenes
A:Reference number: JE0061
A:Accession: A38835
A:Molecule type: DNA
A:Residues: 1-411 <KAN>
A:Cross-references: UNIPROT:P16962; EMBL:X55659; NID:g47340; PIDN:CAA39192.1; PID:g47341
R:Kanaoka, M.; Negoro, T.; Kawanaka, C.; Agui, H.; Nabeshima, S. Agric. Biol. Chem. 55, 743-750, 1991
A:Title: Streptococcal antitumor protein: expression in Escherichia coli cells and properties
A:Reference number: JH0364; MUID:91234346; PMID:1368629
A:Accession: A33225
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-57 <KA2>
C:Superfamily: arginine deiminase arca

Query Match 32.0%; Score 679; DB 2; Length 411;
Best Local Similarity 39.4%; Pred. No. 1.5e-40;
Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;
QY 11 IHVYSEIGELETVLVHPGREGIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGI 70
Db 7 IHVYSEIGKUKVLLHHPGKEINLMPDYLERLLFDDIPLEDAQKEHDAPQALDEGI 66
QY 71 NVVELTDLVAETDYLASKAAKEFIETFLBETVPLTEANKKAVRAPL 129
Db 67 EVLYLETAAES--LVTPEIREAFIDEYLSE--ANIRGRATKKAIRELLMAIEDNQELIEK 123
QY 130 MMSGITKYELG-----VESENELIVDPMPNLVFTTRDPFASVGVNGVTIHPMYRI 177
Db 124 TWAGVQKSELPEIPASEKGTDLVESNYPPAIDMPNLVFTTRDPFATIGTGSINHPSE 183
QY 178 VRRRETLFARFVRNHPKLV--VKTPMYDPAKMPVIEGGDVFIYNNETLVVGVSERTDLD 235
Db 184 TRRETLVYKGIIFTHPIYGGKVPWYDRNETRIEGGDELVLSDKDLVAVGISQRIDAA 243
QY 236 TITLAKNIKANKVEFKRIIVAINVPKWTNLMHLDITWLTMDKNKFLYSYP--IANDVFKFW 294
Db 244 SIEKLLVNI--FKQNLGFKKVLAFEPANRRKFMHLDITVFTWVDYDKFTIHPHIEIGDLRV-- 300
QY 295 DYDLVNGGAEPOPQNLGLPLDKLLASIIINKEPV--LIPDGAGATEMEIARETFTDGTNYL 353
Db 301 -YSVTYDNEHLHTVBEKGDILAEALLAANLGVKEKVDLIRCGGDNL--VAAGREQWNGDSNTL 357
QY 354 AIKPGGLVIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMGNARCMSPLSRKDV 407
Db 358 TIAPGVVVVYNNRTIITNAILSEKGLKLIKHGSELVGRGGPRCMSPFPFEREDI 411

RESULT 4
D95251
arginine deiminase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95251
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide

| | | | | | | | | | |
|---|------|---|-----|------------|------|--------|-----|------|-----|
| Matches | 148; | Conservative | 85; | Mismatches | 155; | Indels | 27; | Gaps | 10; |
| Qy | 11 | IHYVSIGELETVLVHVEPGREIDYITPARDELFLSAILESHDKARKEHQSFKVMKMDRGI | 70 | | | | | | |
| Db | 6 | IKVNSBIGALKTVLLKRPKGELNLPDYLDGLGDDIPYLEVAQKEHDFHAQVLRBEVG | 65 | | | | | | |
| Qy | 71 | NVVELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAPLLSKPHEMVEPM | 130 | | | | | | |
| Db | 66 | EVLYLEKLAABS--IENPQVRSEFIDDLVAESKKTIL-GHEEIEKTLFATLSNQELVDKI | 122 | | | | | | |
| Qy | 131 | MSGITTKYELG-----VESENELIVDPMPNLVYFTRDPFASVGVNGVTTHFWRYIVRRR | 181 | | | | | | |
| Db | 123 | MSGVRKEENPKCTHLVEYMDXKPYFLDPMPNLYFTRDPOASIGHGIIITNRHWRARRR | 182 | | | | | | |
| Qy | 182 | ETLPARFVFRNHPKL--VKTPTWYDPAKMKPIEGGDVFIYNNETLVVGVSERTDLDTITL | 239 | | | | | | |
| Db | 183 | ESIFIQIVVKKHPRFKDANIPIWLDRDCPNIEGGDELVLSDKVLATIGVSERTSAQAIK | 242 | | | | | | |
| Qy | 240 | LAKNIKANKEVEKRLVAINVPRKWTNLMHLDTWLTMLDKNKP-LYSPIAN-----DVPEKF | 293 | | | | | | |
| Db | 243 | LARRIFENPOATPKVVAIBIPTSRTFMHLDVTFMTIDYDKFTMHSAILKABGNMNIPI-I | 301 | | | | | | |
| Qy | 294 | WDYDLVNGGAEPQPLNGLPLDKLLASIIINKSPV-LIPIGCAGATEMEIAETNFDCGTNY | 352 | | | | | | |
| Db | 302 | IEYDVNVKDAIKQSSH---LKDTELDVLGIDDIQIPTGNGDV--IDGAREQWNGDSNT | 356 | | | | | | |
| Qy | 353 | LAIKPGLVIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCWSMPLSRKDV | 407 | | | | | | |
| Db | 357 | LCIRPGVVVYDRNYSVNDLLRQKGIKVIISGSELVGRGGPRCWSQPLFREDI | 411 | | | | | | |
| RESULT 6 | | | | | | | | | |
| AE1437 | | | | | | | | | |
| arginine deiminase homolog lin0036 [imported] - Listeria innocua (strain Clip11 | | | | | | | | | |
| C:Species: Listeria innocua | | | | | | | | | |
| C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 | | | | | | | | | |
| C:Accession: AE1437 | | | | | | | | | |
| R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; | | | | | | | | | |
| ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; | | | | | | | | | |
| D.; Jones, L.M.; Karst, U. | | | | | | | | | |
| Science 294, 849-852, 2001 | | | | | | | | | |
| A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkar, G.; Madueno, E.; Maitournan, | | | | | | | | | |
| Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; | | | | | | | | | |
| A>Title: Comparative genomics of Listeria species. | | | | | | | | | |
| A:Reference number: AB1077; MUID:21537279; PMID:11679669 | | | | | | | | | |
| A:Accession: AE1437 | | | | | | | | | |
| A>Status: preliminary | | | | | | | | | |
| A:Molecule type: DNA | | | | | | | | | |
| A:Residues: 1-408 <GLA> | | | | | | | | | |
| A:Cross-references: UNIPROT:Q92FR7; GB:AL592022; PIDN:CAC95269.1; PID:gl6412457 | | | | | | | | | |
| A:Experimental source: strain Clip11262 | | | | | | | | | |
| C:Genetics: | | | | | | | | | |
| A:Gene: lin0036 | | | | | | | | | |
| C:Superfamily: arginine deiminase arca | | | | | | | | | |
| Query Match 30.1%; Score 638; DB 2; Length 408; | | | | | | | | | |
| Best Local Similarity 38.5%; Pred. No. 1.2e-37; | | | | | | | | | |

Db 177 PARRRESFIELLKHHPFRSSQETPIWSGREPEPPLEGGDELINBETVLVGSERTDA 236
Qy 235 DTITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVPKF 293
Db 237 RAVERLABSL-FSRAPKIKRVLAAEIPETRSFMHLDVTVMVNFPAQFTIHPAIQOQOEL 295
Qy 294 WDYDL--VNGGAEPQQLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMETARETNDGT 350
Db 296 NVYILEKSENGLEITPRRD---FKRVIAEVLGVPEVDFIPCGGBDV--IVSAREQWMDGA 350
Qy 351 NYLAIKPLGVICYDRNEKTNAALKAAGITVLPFFHGNOLSLGMGNARCMSPLSRKDVK 408
Db 351 NTLAIAPGEVITYDRNVHSNDLLRKAGIKVHEVISSELSRGRGPRCMTWPIITGNLK 408
RESULT 7
AD1080
arginine deiminase homolog lmo0043 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1080
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeschez
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-410 <G>A
A;Cross-references: UNIPROT:Q8VASO; GB:NC_003210; PIDN:CAC98258.1; PID:g16409402; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0043
C;Superfamily: arginine deiminase arca
Query Match 29.8%; Score 632; DB 2; Length 410;
Best Local Similarity 37.5%; Pred. No. 3.2e-37;
Matches 156; Conservative 78; Mismatches 152; Indels 30; Gaps 11;
Qy 11 IHVYSEIGELTVLHVPGRIDYITPARDELIFSAILSHDARKEHQSPVKIMKDRGI 70
Db 7 LNIITSEIGKQTVLVKRGPSLENITPEYLSLFDIPYLKMMQKSHDFFAKTRDSNI 66
Qy 71 NVBELTDLVAETVYDLASKAAKEEFTETFLTEETVPVLTANKKA--VRAFLLSKPTHEMVE 128
Db 67 EVLYLEKLAALREANN--KESFLTKIKES---NQMDSEALYVRDYLMSFDEEEMIR 120
Qy 129 FPMGSGITKYLGVSENEL-----IVDPMPNLYFTRDPPFASVGVNGVTIHFMYIY 178
Db 121 KLMSGLKKESEIPERKKHNLNEMDEQYPPFLDPLNLYFTRDPAAVIENGVTINRMFQPA 180
Qy 179 RRETLFARFVRNHPKLVK--TPWYDPAKMPDIEGDVFIYNNETLVVGVSERTDLD 236
Db 181 RRRESFIELLKHHPFRSSQETPIWSGREPEPPLEGGDELINBETVLVGVSERTDARA 240
Qy 237 ITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVPKFWMD 295
Db 241 VERLAESL-FNRSPKIKRVLAVEIPETRSFMHLDVTVMVNFPAQFTIHPAIQOQOELNI 299
Qy 296 YDL--VNGGAEPQQLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMETARETNDGTNY 352
Db 300 YILEKSENGLEITPRRD---FQVIAEVLDEPFDIFPCGGBDV--IVSAREQWMDGANT 354
Qy 353 LAIKPGVIGYDRNEKTNAALKAAGITVLPFFHGNOLSLGMGNARCMSPLSRKDVK 408
Db 355 LAIAPGEVITYDRNVHSNDLLRSAGIKVHEVISSELSRGRGPRCMTWPIVLENLK 410

RESULT 8

E86879
arginine deiminase (EC 3.5.3.6) [imported] - Lactococcus lactis subsp. lactis (strain IL
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86879
R;Boloian, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-410 <S>O
A;Cross-references: UNIPROT:P58013; GB:AE005176; PID:g12725086; PIDN:AAK06135.1; GSPDB:GN
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arca
C;Superfamily: arginine deiminase arca
C;Keywords: hydrolase
Query Match 29.8%; Score 631.5; DB 2; Length 410;
Best Local Similarity 37.3%; Pred. No. 3.4e-37;
Matches 156; Conservative 70; Mismatches 163; Indels 29; Gaps 6;
Qy 9 NGIHVYSEIGELTVLHVPGRIDYITPARDELIFSAILSHDARKEHQSPVKIMKDR 68
Db 3 NGINVNSEIGKLSVILLHRPGEVENITPTMKQLLFDIPYLKIAQKEHDFFAQTLRDN 62
Qy 69 GINWVELTDLVAETVYDLASKAAKEEFTETFLTEETVPVLTANKKAVRAPLLSK 121
Db 63 GAETVYIENLATEVFEKSSE--TKEEFLSHLLHAGVRPGTYDGLTE-----YLTSM 113
Qy 122 PTHMVEFMMSGITKVEL-----GVSENELIVDPMPNLYFTRDPPFASVGVNGVT 170
Db 114 STKDMVEKIYAGVRKNEIDIKRTALSDMGSDAENFYLNPLFNAYFTRDPQASMGVMT 173
Qy 171 IHFMRYIVRRRETLFARFVRNHPKLVKTPWYDPAKMPDIEGDVFIYNNETLVGVSE 230
Db 174 INKOTFPARQPESLITEYVYMANHPRFDTPIWDRNHTTRIEGGDELINLTKTTVAIGVSE 233
Qy 231 RTDLDTITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDV 290
Db 234 RTSKTIQNLAKELFANPLSTFDTVLAVEIPHNHMMHLDVTVMINHDDQFTVFPGIMDG 293
Qy 291 FXFDVLDLVNGAEPQQLNGL-PLDKLLASIIINKEPVLIPIGAGATEMEIARETNFDG 349
Db 294 AGNINVFILRPGKDDVEIEHILTDLKAALKKVLNLSLSELDLIECGAG-DPIAAPREQWNDG 352
Qy 350 TNYLAIKPGVIGYDRNEKTNAALKAAGITVLPFFHGNOLSLGMGNARCMSPLSRKDV 407
Db 353 SNTLAIAPGEIVTYDRNYVTVELLKEHGKIKVHEILSELGRGGRGARCMSQPLWREDL 410
RESULT 9
T46741
arginine deiminase (EC 3.5.3.6) [validated] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46741
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C
J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of t
A;Reference number: 223141; MUID:98361904; PMID:9696763
A;Accession: T46741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <Z>N
A;Cross-references: UNIPROT:O53088; EMBL:AJ001330; NID:g2764610; PIDN:CAA04682.1; PID:92
C;Genetics:
A;Gene: arca
C;Function:
A;Description: EC 3.5.3.6 [validated, MUID:98361904]
A;Pathway: arginine catabolism

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB1060

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-406 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06927.1; PID:g16505575; GSPDB:GN00176

C;Genetics:

A;Gene: STV4805

C;Superfamily: arginine deiminase arca

C;Keywords: hydrolase

Query Match 25.0%; Score 531; DB 2; Length 406;

Best Local Similarity 32.9%; Pred. No. 4.4e-30;

Matches 136; Conservative 74; Mismatches 172; Indels 32; Gaps 9;

Qy 13 VYSGELETVLVHVEGREIDYITPARLDELLFSAILESHDARKEHQSFKVMKDRGINV 72

Db 6 VSGEIGQLRSVMLHRPNLSKRLTPSNCQELLFDDVLSVERAGEHDIPANTLRQOGIEV 65

Qy 73 VELDLVAETDYLASKAAKEEFIEETLEETVPLTEANKKAVRAFLSKPETHENVEFMS 132

Db 66 LLLDLTLTQTLUDVAD--AKAWLLDTQISDY--RLGPTFAADIRAWLADMPHRELARLSG 121

Qy 133 GITKYEELGVSE-----NELIVDPMPNLYETRDPFASVGVNGVTIHFWRVIYVRRET 183

Db 122 GLTYGEIPASIKNMVVDTHINDIFMKPLPNHLETRTSCWYNGVSNPMAKPARORET 181

Qy 184 LFARFVRNHPKLVKTPWY-----YDPAMQPIEGGDVFIYNNETLVGVGSERTDL 234

Db 182 NNLRAIYRWHPQFADGDFIKYFGDENINYDHA---TLEGGDVLVIGRAVLIGMSERTTP 238

Qy 235 DTITLLAKNIKANKVEFKRIIVAINPKWTNLMHLDLTMLDKKNKFLYSPIANDVFKF 293

Db 239 QGVFLQAALPKHQAB--RVIAVELPKHRSCHMLDTVMTHIDITFSVPEVVRPDVQC 296

Qy 294 WDYDLVNGGAPQPLNGLPLDKLLASIIINKEPVLPIPGAGAGATEMIARETNPDTGNYL 353

Db 297 W--TLTPDGRGLKRTQESTLVHALETALGIDQVRLITTGDAFEAE--REQNDANNVL 352

Qy 354 AIKPLGVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407

Db 353 TLREPGVVGVERNIWTNEKYDKAGITVLPFGDLGRGRGCARCMSCLPDRDGI 406

RESULT 13

F82323

arginine deiminase VC0423 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: F82323

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82323

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-407 <HEI>

A;Cross-references: UNIPROT:Q9KU02; GB:AE004130; GB:AE003852; NID:g9654845; PIDN:AAF9359

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0423

A;Map position: 1

C;Superfamily: arginine deiminase arca

Query Match 23.7%; Score 502.5; DB 2; Length 407;

Best Local Similarity 31.8%; Pred. No. 4.7e-28;

Matches 134; Conservative 79; Mismatches 171; Indels 37; Gaps 9;

Qy 9 NGIHVYSEIGELETVLVHVEGREIDYITPARLDELLFSAILESHDARKEHQSFKVMKDR 68

Db 2 NRIYVGSEVQGLRVILNRPERALTHLTFSNCHLELLFDDVLVAEAGVEHDAFANTLRQ 61

Qy 69 GINVELTDLVAETYDLASKAAKEEFIEETLEETVPLTEANKKAVRAFLSKPETHMVE 128

Db 62 DVEVLLHDLLEET--LAIPARQWLLNTQISDFRFGPTFA--RELHALNLHLDHHLTT 117

Qy 129 FMMSGITKVELGVSE-----ELIVDPNPLYETRDPFASVGVNGVTIHFMYIVR 179

Db 118 LLGGGLAFSELHLESMLPQMRQPLDFVIEPLNHLFTRDTSCWYGVGSVSLNPMKMPAR 177

Qy 180 RRETLFARFVRNHPKLVKTPW-----YDPAMQPIEGGDVFIYNNETLVGVSE 230

Db 178 QRETNHLRAIYRWHPPIFAQHPFIHYGIDDLHDVNA---NIEGDDVLVIGKGAVLGMSE 234

Qy 231 RTDLDTITLLAKNIKANKVEFKRIIVAINPKWTNLMHLDLTMLDKKNKFLYSPIANDV 290

Db 235 RTSPOGVENLAAL--FKHQASKVIATNLPKHSRCHMLDTVMTHMDVDTFSVYP---EV 289

Qy 291 FKWDYDLVNGGAPQPLNGLPLDKLLASIIINKEPVL-----IPGGAGATEMIARETN 346

Db 290 MR---KDLPTWRLUTPKGNNGDMRVEQVPSYLHAEQALGVVDYDKIITTGNSYEAREQW 346

Qy 347 FDGTNYLAIKPLGVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKD 406

Db 347 NDANNVLTVKPGVIGYERNVYNEKYDKAGIKVLTIPGNELGRGRGCARCMSCLPDRDG 406

Qy 407 V 407

Db 407 I 407

RESULT 14

S73858

arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)

N;Alternate names: hypothetical protein H10_orf238

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C;Accession: S73858

R;Himmelsreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73858

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-238 <HIM>

A;Cross-references: EMBL:AB000052; GB:U00089; NID:g1674223; PIDN:AAB96180.1; PID:g1674223

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Gene: arca

A;Genetic code: SGC3

C;Keywords: hydrolase

Query Match 23.1%; Score 490; DB 2; Length 238;

Best Local Similarity 50.3%; Pred. No. 1.7e-27;

Matches 97; Conservative 43; Mismatches 47; Indels 6; Gaps 3;

Qy 7 KFNHIVYSEIGELETVLVHVEGREIDYITPARLDELLFSAILESHDARKEHQSFKVMK 66

Db 2 KYN-INVHSEIGQLQTVLVHTPGNEIRRIISPRRLDLSFSAVIEPTAQEHQTFQQLQ 60

Qy 67 DRGINVVELTDLVAETYDLASKAAKEEFIEETLEETVPLTEANKKAVRAFLI---SKPT 123

Db 61 EQNIEVQLTDLTATTTDFDKANATAQNFITELWLDQAEPLKTPHRRKVAQYLLQEAKST 120

Qy 124 HEMVEFPMMSGITKYEELGVSE--ENELIVDPNPLYETRDPFASVGVNGVTIHFMYIVRR 181

Db 121 LSNVSRMGMGIDKRVAAANTINGDFLVDPMNLYETRDPFASIGHISINRMKYLTRR 180

Qy 182 ETLFARFVRNHP 194

Job time : 44 secs

Db 181 ETLFASFIPTTP 193

RESULT 15
C95376

probable arginine deiminase (EC 3.5.3.6) [imported] - Sinorhizobium meliloti (strain 102)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95376
R;Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95376
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Cross-references: UNIPROT:Q92YG5; GB:AE006469; PIDN:AAK65573.1; PID:g14524052; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaullt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: arcA2
A;Genome: plasmid
C;Superfamily: arginine deiminase arca
C;Keywords: hydrolase

Query Match 22.8%; Score 484; DB 2; Length 419;
Best Local Similarity 29.1%; Pred. No. 9.9e-27;
Matches 130; Conservative 82; Mismatches 170; Indels 64; Gaps 14;

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Qy 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEEFIEFTLEETVP-----VLTEANKKAV 114
Db 61 FMTKMRDRGVEVEMENLLAQT--VAIPERKWILD---NQVVPNQVGLLELDE-----I 110
Qy 115 RAFLSKPTHEMVEFMWSGITKVEL-----GVESNELIVDPMPNLYFT 158
Db 111 RSYLEGLPDRELAETLIGLSTHEFPETHGGEMLERDAAGVA---EYLLPLPLNTLYT 167
Qy 159 RDPFASVGNQVTIHFVRYVRRRETLFARFVRNHPKLV--KTPWYDPAK---MPIEG 213
Db 168 RDTTCWYGGVTINPLNYPARHEETILATAIYKFPDPFVGKVMVMGEPTTDWGLATLEG 227
Qy 214 GDVFIYNNETLVVGVSERTDLDITLLAKNIKAKKEVEFKRIVAINVPKWTNLMHLDTWL 273
Db 228 GDVMPGKGNVLIGMSERTSRQISLAATLFEKGAQ--RVIVAAMPKLRANHLDTVF 285
Qy 274 TMLDKN-KFLYSPINDVPKFWDYDLVNGAEFPQQLNGPLDLKLASIIIN-----K 324
Db 286 TFADRDCLVIYPIVNEIAF-----SYRFGKPGSLHLKHGRGSFVETVRDALGLK 337
Qy 325 EPVLIPIGGAGATEMETARETNFD-GNYLIAIKPLVIGYDRNEKTNAALKAAGITVLPF 383
Db 338 EMRWETGG----NAYVRRTOTMDSGANLVCLSPGVVLAYDRNTYNTTLRKAGVEVITI 393
Qy 384 HGNQLSLGMCNARCMSPLSRKDKWK 409
Db 394 TGAELGRGCGGHCMTPIIRDADVY 419

Search completed: November 23, 2004, 15:51:55

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 15:45:18 ; Search time 146 Seconds
(without alignments)
992.042 Million cell updates/sec

Title: US-10-674-666-1
Perfect score: 2120
Sequence: 1 MSVFSKFNHIVSEIGLE.....LGMNARCMSPLSRKDKVKW 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 2120 | 100.0 | 409 | 16 | US-10-674-666-1 |
| 2 | 2116 | 99.8 | 409 | 16 | US-10-674-666-2 |
| 3 | 2112 | 99.6 | 409 | 16 | US-10-674-666-3 |
| 4 | 2108 | 99.4 | 409 | 16 | US-10-674-666-4 |
| 5 | 1797.5 | 84.8 | 409 | 16 | US-10-674-666-7 |
| 6 | 1793.5 | 84.6 | 409 | 16 | US-10-674-666-9 |
| 7 | 1793.5 | 84.6 | 409 | 16 | US-10-674-666-10 |
| 8 | 1789.5 | 84.4 | 409 | 16 | US-10-674-666-8 |
| 9 | 1764.5 | 83.2 | 410 | 15 | US-10-674-666-5 |
| 10 | 1763.5 | 83.2 | 410 | 15 | US-10-343-175-10 |
| 11 | 1760.5 | 83.0 | 410 | 16 | US-10-674-666-6 |
| 12 | 707.5 | 33.4 | 410 | 14 | US-10-369-493-16696 |
| 13 | 681.5 | 32.1 | 413 | 16 | US-10-674-666-19 |

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|----|-------|------|------|----|----------------------|-------------------|
| 14 | 679 | 32.0 | 411 | 16 | US-10-674-666-13 | Sequence 13, Appl |
| 15 | 670.5 | 31.6 | 408 | 16 | US-10-674-666-20 | Sequence 20, Appl |
| 16 | 655 | 30.9 | 413 | 16 | US-10-674-666-18 | Sequence 18, Appl |
| 17 | 651.5 | 30.7 | 409 | 16 | US-10-674-666-14 | Sequence 14, Appl |
| 18 | 631.5 | 29.8 | 410 | 14 | US-10-369-493-18511 | Sequence 18511, A |
| 19 | 625 | 29.5 | 409 | 16 | US-10-674-666-21 | Sequence 21, Appl |
| 20 | 612.5 | 28.9 | 410 | 16 | US-10-674-666-15 | Sequence 15, Appl |
| 21 | 600.5 | 28.3 | 409 | 16 | US-10-674-666-16 | Sequence 16, Appl |
| 22 | 532 | 25.1 | 403 | 14 | US-10-369-493-8351 | Sequence 8351, Ap |
| 23 | 532 | 25.1 | 403 | 14 | US-10-369-493-715 | Sequence 715, App |
| 24 | 514 | 24.2 | 409 | 14 | US-10-156-761-9857 | Sequence 9857, Ap |
| 25 | 486.5 | 22.9 | 418 | 14 | US-10-369-493-13732 | Sequence 13732, A |
| 26 | 476 | 22.5 | 399 | 14 | US-10-369-493-7149 | Sequence 7149, Ap |
| 27 | 467 | 22.5 | 401 | 14 | US-10-369-493-4394 | Sequence 4394, Ap |
| 28 | 467 | 22.5 | 403 | 14 | US-10-369-493-4661 | Sequence 4661, Ap |
| 29 | 457 | 22.0 | 403 | 14 | US-10-369-493-7420 | Sequence 7420, Ap |
| 30 | 457 | 22.0 | 403 | 14 | US-10-369-493-12226 | Sequence 12226, A |
| 31 | 220 | 10.4 | 415 | 14 | US-10-369-493-11106 | Sequence 11106, A |
| 32 | 154 | 7.3 | 81 | 9 | US-09-867-550-164 | Sequence 164, App |
| 33 | 136 | 6.4 | 105 | 15 | US-10-424-599-164647 | Sequence 164647, |
| 34 | 113.5 | 5.4 | 1270 | 14 | US-10-032-585-7127 | Sequence 7127, Ap |
| 35 | 113 | 5.3 | 743 | 15 | US-10-282-122A-74773 | Sequence 74773, A |
| 36 | 109 | 5.1 | 453 | 15 | US-10-282-122A-42589 | Sequence 42589, A |
| 37 | 105 | 5.0 | 580 | 16 | US-10-674-666-17 | Sequence 17, Appl |
| 38 | 104.5 | 4.9 | 740 | 15 | US-10-282-122A-72237 | Sequence 72237, A |
| 39 | 104.5 | 4.9 | 1057 | 15 | US-10-282-122A-70305 | Sequence 70305, A |
| 40 | 104 | 4.9 | 4688 | 15 | US-10-282-122A-76865 | Sequence 76865, A |
| 41 | 103 | 4.9 | 502 | 15 | US-10-282-122A-54571 | Sequence 54571, A |
| 42 | 103 | 4.9 | 772 | 13 | US-10-121-032-28 | Sequence 28, Appl |
| 43 | 103 | 4.9 | 772 | 14 | US-10-093-037-28 | Sequence 28, Appl |
| 44 | 103 | 4.9 | 800 | 14 | US-10-228-063-3 | Sequence 3, Appl |
| 45 | 103 | 4.9 | 825 | 14 | US-10-228-063-24 | Sequence 24, Appl |

ALIGNMENTS

RESULT 1
US-10-674-666-1
; Sequence 1, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PH05001-300
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-1

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|-----------------------|--------|--|----------|------------|----|--------|-----|
| Query Match | 100.0% | Score | 2120 | DB | 16 | Length | 409 |
| Best Local Similarity | 100.0% | Pred. No. | 4.9e-186 | | | | |
| Matches | 409 | Conservative | 0 | Mismatches | 0 | Indels | 0 |
| | | Gaps | 0 | | | | |
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| Db | 1 | MSVFSKFNHIVSEIGLETVLVHVPQREIDYITPARLDELLFSAILES HDARKEHQS | 60 | | | | |
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| Db | 61 | FKVIMKDRGINVVELTDLVAETIDYDLASKAAKEFIETFTLEETVPVLTEANKKAVRAFLLS | 120 | | | | |
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| Db | 121 | KPTHEVPEFMSGITYKELGVSENELIVDPNPNLYFTDRPPASVGVNGVTIHFMYIVRR | 180 | | | | |

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RESULT 2
US-10-674-666-2
; Sequence 2, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-2

Query Match 99.8%; Score 2116; DB 16; Length 409;
Best Local Similarity 99.8%; Pred. No. 1.1e-185;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
QY 61 FVKIMKORGINNVVELTDLVAETYDLASKAAKEEFIEETVLPVLT EANKKAVRAFLS 120
DB 61 FVKIMKORGINNVVELTDLVAETYDLASKAAKEEFIEETVLPVLT EANKKAVRAFLS 120
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DB 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDKVKW 409

RESULT 3
US-10-674-666-3
; Sequence 3, Application US/10674666

Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-3

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Best Local Similarity 99.8%; Pred. No. 2.7e-185;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
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DB 61 FVKIMKORGINNVVELTDLVAETYDLASKAAKEEFIEETVLPVLT EANKKAVRAFLS 120
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QY 181 RETLFAFVFRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240
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RESULT 4
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; Sequence 4, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-4

Query Match 99.4%; Score 2108; DB 16; Length 409;
Best Local Similarity 99.5%; Pred. No. 6.2e-185;
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5
US-10-674-666-7
; Sequence 7, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOS0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-7

Query Match 84.8%; Score 1797.5; DB 16; Length 409;
Best Local Similarity 84.4%; Pred. No. 2.2e-156;
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;
QY 1 MSVFDKFNHGIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHOS 60
Db 1 MSVFDKFNHGIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVLDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVLDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120
QY 121 KPTHEMVFEFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYVR 179
Db 121 KPTHEMVFEFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYVR 180
QY 180 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 239
Db 180 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240
QY 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 299
Db 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 300

QY 300 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359
Db 301 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409
RESULT 6
US-10-674-666-9
; Sequence 9, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOS0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-9

Query Match 84.6%; Score 1793.5; DB 16; Length 409;
Best Local Similarity 84.1%; Pred. No. 5.2e-156;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;
QY 1 MSVFDKFNHGIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHOS 60
Db 1 MSVFDKFNHGIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVLDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVLDLASKAAKEBFIEFTLEETVPVLTTEANKKAVRAFLLS 120
QY 121 KPTHEMVFEFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYVR 179
Db 121 KPTHEMVFEFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYVR 180
QY 180 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 239
Db 180 RETLFAFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240
QY 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 299
Db 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDITWLTMDKNKFLYSPANDVFKFWDYDLV 300
QY 300 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359
Db 301 NGGAEPQOLNGLPLDKLASIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 7
US-10-674-666-10
; Sequence 10, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOS0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29

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; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-10

Query Match      84.6%; Score 1793.5; DB 16; Length 409;
Best Local Similarity 84.8%; Pred. No. 5.2e-156;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB 1 MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEQS 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
DB 61 FVAILKANDINVVETIDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120

QY 121 KPT-HEMVPEFMSGITKYELGVSENELIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYR 179
DB 121 KTSRKLVELMMAGITKYDLGVADHELIYDPMPLNYFTRDPPASVGVNGVTIHFMYIYR 180

QY 180 REETLFAFVRPNHPKLVNTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITL 239
DB 180 REETLFAFVRPNHPKLVNTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITL 240

QY 240 LAKNIVANKEVEKRIIVAINVPKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV 299
DB 240 LAKNIVANKEVEKRIIVAINVPKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPQPLNGPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGL 359
DB 300 NGGAEPQPLNGPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIRPGV 360

QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
DB 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 9
US-10-674-666-5
; Sequence 5, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHO0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arginini
US-10-674-666-5

Query Match      83.2%; Score 1764.5; DB 16; Length 410;
Best Local Similarity 82.0%; Pred. No. 2.4e-153;
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB 1 MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
DB 61 FVAILKANDINVVETIDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120

QY 121 KPT-HEMVPEFMSGITKYELGVSENELIVDPMPNLYFTRDPPASVGVNGVTIHFMYIYR 179
DB 121 KTSRKLVELMMAGITKYDLGVADHELIYDPMPLNYFTRDPPASVGVNGVTIHFMYIYR 180

QY 180 REETLFAFVRPNHPKLVNTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITL 239
DB 180 REETLFAFVRPNHPKLVNTPWYDPAKMPLEGDVFYNNETLVVGVSERTDLDITL 240

QY 240 LAKNIVANKEVEKRIIVAINVPKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV 299
DB 240 LAKNIVANKEVEKRIIVAINVPKWTNLMHLDITLWMLDKNKFYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPQPLNGPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGL 359
DB 300 NGGAEPQPLNGPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIRPGV 360

QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409
DB 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 8
US-10-674-666-8
; Sequence 8, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHO0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-8

Query Match      84.4%; Score 1789.5; DB 16; Length 409;
Best Local Similarity 83.9%; Pred. No. 1.2e-155;
Matches 343; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB 1 MSVDSKFGNGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEQS 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
DB 61 FVAILKANDINVVETIDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
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Db 361 VIGYSRNEKTNAALEAAGIKVLPFHGNQLSLGNGNARCMPLSRKDVVKW 410
RESULT 10
US-10-343-175-10
; Sequence 10, Application US/10343175
; Publication No. US20040096437A1
; GENERAL INFORMATION:
; APPLICANT: Angioblab, Inc.
; TITLE OF INVENTION: The pharmaceutical composition containing arginine deiminase for
; inhibiting angiogenesis
; FILE REFERENCE: PCA/KR01/01281
; CURRENT APPLICATION NUMBER: US/10/343,175
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 10
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acids coding Mycoplasma Arginine Deiminase
US-10-343-175-10
Query Match 83.2%; Score 1763.5; DB 15; Length 410;
Best Local Similarity 82.0%; Pred. No. 3e-153;
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;
QY 1 MSVFSKFGNGIHVYSEIGLETVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
DB 1 MSVFSKFGNGIHVYSEIGLESVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTANKKAVRAFLLS 120
DB 61 FVAELKANDINVVELLDLVAETDYDLASQAQKLIIEFLEDSSEPVLSSEHVVVRNFKLA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHFMYIYVR 179
DB 121 KTSRELVEIMMAGITKYDLGIEADHELIVDPMPNLYFTRDPFASVGVNGVTIHFMYIYVR 180
QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPTEGGDVFTYNNETLVVGVSRERDLDITTL 239
DB 181 QRETLFSRFVSNHPKLINTPWYDPSLKSLIEGGDVFTYNNETLVVGVSRERDLDITTL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKDKFLYSPINDVVKFWDYDLV 299
DB 241 LAKSIVANKECFKRIIVAINVPKWTNLMHLDTWLMDKDKFLYSPINDVVKFWDYDLV 300
QY 300 NGGABPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359
DB 301 NGGABPQPVENGPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMPLSRKDVVKW 409
DB 361 VIGYSRNEKTNAALEAAGIKVLPFHGNQLSLGNGNARCMPLSRKDVVKW 410
RESULT 11
US-10-674-666-6
; Sequence 6, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOR001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 410
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; TYPE: PRT
; ORGANISM: Mycoplasma arginini
US-10-674-666-6
Query Match 83.0%; Score 1760.5; DB 16; Length 410;
Best Local Similarity 81.7%; Pred. No. 5.7e-153;
Matches 335; Conservative 38; Mismatches 36; Indels 1; Gaps 1;
QY 1 MSVFSKFGNGIHVYSEIGLETVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
DB 1 MSVFSKFGNGIHVYSEIGLESVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTANKKAVRAFLLS 120
DB 61 FVAELKANDINVVELLDLVAETDYDLASQAQKLIIEFLEDSSEPVLSSEHVVVRNFKLA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVNGVTIHFMYIYVR 179
DB 121 KTSRELVEIMMAGITKYDLGIEADHELIVDPMPNLYFTRDPFASVGVNGVTIHFMYIYVR 180
QY 180 RRETLPARFVRNHPKLVKTPWYDPAKMPTEGGDVFTYNNETLVVGVSRERDLDITTL 239
DB 181 QRETLFSRFVSNHPKLINTPWYDPSLKSLIEGGDVFTYNNETLVVGVSRERDLDITTL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKDKFLYSPINDVVKFWDYDLV 299
DB 241 LAKNIVANKECFKRIIVAINVPKWTNLMHLDTWLMDKDKFLYSPINDVVKFWDYDLV 300
QY 300 NGGABPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGL 359
DB 301 NGGABPQPVENGPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMPLSRKDVVKW 409
DB 361 VIGYSRNEKTNAALEAAGIKVLPFHGNQLSLGNGNARCMPLSRKDVVKW 410
RESULT 12
US-10-369-493-16696
; Sequence 16696, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16696
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16696
Query Match 33.4%; Score 707.5; DB 14; Length 410;
Best Local Similarity 40.9%; Pred. No. 3.9e-56;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;
QY 11 IHVYSEIGLETVLVHVEPGREIDYITPARLDELLFSAILES HDARKEHQS FVKIMKDRGI 70
DB 5 IHVTSIGELQIVLLKRGKEVENLTPDYLLQQLFDDIPYLPLOKEHDYFAQTLANRGV 64
QY 71 NVVELTDLVAETDYDLASKAAKEEFIEETLEETVPVLTANKKAVRAFLLSKPHWEFPM 130
DB 65 EVLYLEKAAEA--LVDDKRLREFVDRLKEGQADVNVAH--QTLKEYLLSFSNEELIQKI 121
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QY 131 MSGITK-----YELGVSENELIVDPMPNLYFTRDPASVGVGVTIHPMYIVR 179
Db 122 MGVKNEIETSKTHLYEL-MEDHYFFYLDPMNLYFTRDPASVGVGVTIHPMYIVR 180
QY 180 RRETFLARFVRNHPKLVK--TPWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDLDTI 237
Db 181 RRESLFMEYIIKYHPRFAKNVPIWLDRDYKFFIEGGDELILNEETIAGVSARTSAKAI 240
QY 238 TLLAKNTKANKEVEFFKRIIVNPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWY 296
Db 241 ERLAKNL-FGRQNKIKVLAIEIPKCRAFMHLDTVFTMVDYDKFTIHPAIGQKGNMNIY 299
QY 297 DLVNGGAEPQOL-NGPLDKLASIIN-KEPVLPIPGGAGATEMETARETNFDGTNYLA 354
Db 300 ILEKGSDEETLKTHRTSLMEALKEVLGLSELVLIPCGGDV--IASAREQWNDGNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFPHGNQLSLGMGNARCMSPLSRKDV 407
Db 358 IAPGVVVYDRNVVSNLTREHGIEVIEVLSSLSRGRGPRCWSMPIVRKDI 410

RESULT 13
US-10-674-666-19
; Sequence 19, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-674-666-19

Query Match 32.1%; Score 681.5; DB 16; Length 413;
Best Local Similarity 38.4%; Pred. No. 9.6e-54;
Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;

QY 11 IHVYSIGELETVLVHEPGREIDYITPARDELFSAILSHDARKEHQSFKVIMKDRGI 70
Db 7 IHVYSIGPLKTYMLKRPGRLENLTPEYLERLLFDDIPFLPAVQKEHQDQFAETLKQQA 66
QY 71 NVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTTEANKKAVRAFLLSKPTHEMVFE 130
Db 67 EVLYLEKLTAEALDDA--IVREQIDELLTESKADINGAYDR-LKSEFLTFDADSWEQV 123
QY 131 MSGITKVELGVSENEL-----IVDPMNLYFTRDPFASVGVGVTIHPMYIVR 180
Db 124 MSGIRKNELEREXKSHLHMLHEDHYPPYLDPMNLYFTRDPAAAGISGLTINKMKEPAR 183
QY 181 RETLFAFVRNHPKLV--KTPWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDLDTI 238
Db 184 RESLFMYIINHPRFKGHEIPVWLDORDFKFNIEGGDELVLNEETVAIGVSERTTAQAE 243
QY 239 LLAKNITKANKEVEFFKRIIVNPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWYDL 298
Db 244 RLVRNL-FQQRIRRVLAIEIPKSRAFMHLDTVFTMVDYDKFTIHPAQI----- 292
QY 299 VNGGAEPPQNLGLPDLKLLASIIINKEPVLIP-----IGGAGATEMIARE 344
Db 293 ---GPEGDMRIFVLERGKTADEIHTTEHNHLPVLRKTLGLSDVNLIFCGGGEIASARE 349
QY 345 TNPDGTNYLAIKPGLVIGYDRNEKTNAAKAGITVLPFPHGNQLSLGMGNARCMSPLSR 404
Db 350 QWNDGNTLAIAPGVVVYDRNVYISNRECUQGIKVIETPSGELSRGRGPRCWSMPLYR 409
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QY 405 KDVK 408
Db 410 EDVK 413

RESULT 14
US-10-674-666-13
; Sequence 13, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-674-666-13

Query Match 32.0%; Score 679; DB 16; Length 411;
Best Local Similarity 39.4%; Pred. No. 1.6e-53;
Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;

QY 11 IHVYSIGELETVLVHEPGREIDYITPARDELFSAILSHDARKEHQSFKVIMKDRGI 70
Db 7 IHVYSIGKLKKVLLHRPKGEIENLMPDYLERLLFDDIPPLEDAQKEHDAFAQALRDEGI 66
QY 71 NVVELTDLVAETVDLASKAAKEEFITFLEETVPVLTTEANKKAVRAFLLS-KPTHEMVFE 129
Db 67 EVLYLETLAAES--LVTPEIREAFIDEYLSE-ANIRGRATKKAIRELLMAIEDNQELIEK 123
QY 130 MMSGITKYELG-----VSENELIVDPMNLYFTRDPFASVGVGVTIHPMYI 177
Db 124 TWAGVQSELPEIPASEKGLTDLVESNYPFADPMNLYFTRDPFATIGVSNLHMFSE 183
QY 178 VRRRETFLARFVRNHPKLV--VKTWYDPAKMPFIEGGDVFIYNNETLVVGVSERTDLD 235
Db 184 TRNRETLYCKYIFTHPIYGGKVPWYDRNETTRIEGGDELVLKDLAVGLSQRDAA 243
QY 236 TITLAKNTKANKEVEFFKRIIVNPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFW 294
Db 244 SIEKLLVNI-FKQNLGFKVLAFEFANNRKFWHLDTVFTMVDYDKFTIHPIEGDLRV-- 300
QY 295 DYDLVNGGAEPQQLNGLPLDKLLASIIINKEPVL-LIPIGGAGATEMEIARETNFDGTNYL 353
Db 301 -XSVTYDNEELHIVEEGDLAEALLANLGVKVDLIRCGDNL--VAAGREQWNDGNTL 357
QY 354 AIKPGLVIGYDRNEKTNAAKAGITVLPFPHGNQLSLGMGNARCMSPLSRKDV 407
Db 358 TIAPGVVVYNNRTIINALESKGLKLIKHGSELVRGRGPRCWSMPPPEREDI 411

RESULT 15
US-10-674-666-20
; Sequence 20, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US 60/427,497
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
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OM protein - protein search, using sw model

Run on: November 23, 2004, 15:44:59 ; Search time 39 seconds
(without alignments)
695.489 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVFDKFNHGYVSEIGEL.....LGMGNARCMPLSRKDKVKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2120 | 100.0 | 409 | 3 | US-09-023-809B-3 |
| 2 | 2120 | 100.0 | 409 | 4 | US-09-564-559B-1 |
| 3 | 2120 | 100.0 | 409 | 4 | US-09-723-546-3 |
| 4 | 2116 | 99.8 | 409 | 4 | US-09-564-559B-2 |
| 5 | 2112 | 99.6 | 409 | 4 | US-09-564-559B-3 |
| 6 | 2108 | 99.4 | 409 | 4 | US-09-564-559B-4 |
| 7 | 2098.5 | 99.0 | 410 | 1 | US-08-792-283A-8 |
| 8 | 2098.5 | 99.0 | 410 | 2 | US-09-105-908-8 |
| 9 | 2098.5 | 99.0 | 410 | 3 | US-09-271-713-8 |
| 10 | 1807.5 | 85.3 | 410 | 3 | US-09-023-809B-2 |
| 11 | 1807.5 | 85.3 | 410 | 4 | US-09-723-546-2 |
| 12 | 1793.5 | 84.6 | 409 | 4 | US-09-564-559B-7 |
| 13 | 1789.5 | 84.4 | 409 | 4 | US-09-564-559B-9 |
| 14 | 1789.5 | 84.4 | 409 | 4 | US-09-564-559B-10 |
| 15 | 1785.5 | 84.2 | 409 | 4 | US-09-564-559B-8 |
| 16 | 1765.5 | 83.3 | 410 | 1 | US-08-792-283A-7 |
| 17 | 1765.5 | 83.3 | 410 | 2 | US-09-105-908-7 |
| 18 | 1765.5 | 83.3 | 410 | 3 | US-09-271-713-7 |
| 19 | 1764.5 | 83.2 | 410 | 3 | US-09-023-809B-1 |
| 20 | 1764.5 | 83.2 | 410 | 4 | US-09-723-546-1 |
| 21 | 1746.5 | 82.4 | 409 | 4 | US-09-564-559B-5 |
| 22 | 1742.5 | 82.2 | 409 | 4 | US-09-564-559B-6 |
| 23 | 1732.5 | 81.7 | 410 | 1 | US-08-792-283A-2 |
| 24 | 1732.5 | 81.7 | 410 | 2 | US-09-105-908-2 |
| 25 | 1732.5 | 81.7 | 410 | 3 | US-09-271-713-2 |
| 26 | 1713.5 | 80.8 | 410 | 1 | US-08-792-283A-9 |
| 27 | 1713.5 | 80.8 | 410 | 2 | US-09-105-908-9 |

| | | | | | | |
|----|--------|------|-----|---|---------------------|--------------------|
| 28 | 1713.5 | 80.8 | 410 | 3 | US-09-271-713-9 | Sequence 9, Appli |
| 29 | 1698.5 | 80.1 | 399 | 6 | 5474928-2 | Patent No. 5474928 |
| 30 | 681.5 | 32.1 | 413 | 4 | US-09-723-546-12 | Sequence 12, Appl |
| 31 | 679 | 32.0 | 411 | 4 | US-09-723-546-6 | Sequence 6, Appli |
| 32 | 670.5 | 31.6 | 408 | 4 | US-09-723-546-13 | Sequence 13, Appl |
| 33 | 667.5 | 31.5 | 417 | 4 | US-09-107-532A-6148 | Sequence 6148, Ap |
| 34 | 655 | 30.9 | 413 | 4 | US-09-723-546-11 | Sequence 11, Appl |
| 35 | 652.5 | 30.8 | 409 | 4 | US-09-583-110-4274 | Sequence 4274, Ap |
| 36 | 651.5 | 30.7 | 409 | 4 | US-09-723-546-7 | Sequence 7, Appli |
| 37 | 640.5 | 30.2 | 411 | 3 | US-08-964-652-2 | Sequence 2, Appli |
| 38 | 640.5 | 30.2 | 422 | 3 | US-09-134-001C-2931 | Sequence 2931, Ap |
| 39 | 625 | 29.5 | 409 | 4 | US-09-723-546-14 | Sequence 14, Appl |
| 40 | 618 | 29.2 | 420 | 3 | US-09-134-001C-4427 | Sequence 4427, Ap |
| 41 | 612.5 | 28.9 | 410 | 4 | US-09-723-546-8 | Sequence 8, Appli |
| 42 | 604.5 | 28.5 | 394 | 4 | US-09-710-279-58 | Sequence 58, Appl |
| 43 | 600.5 | 28.3 | 409 | 4 | US-09-723-546-9 | Sequence 9, Appli |
| 44 | 581.5 | 27.4 | 379 | 4 | US-09-134-000C-6027 | Sequence 6027, Ap |
| 45 | 474 | 22.4 | 356 | 4 | US-09-710-279-2488 | Sequence 2488, Ap |

ALIGNMENTS

RESULT 1
US-09-023-809B-3
; Sequence 3, Application US/09023809B
; Patent No. 6183738
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0028
; CURRENT APPLICATION NUMBER: US/09/023,809B
; CURRENT FILING DATE: 2000-02-13
; PRIOR APPLICATION NUMBER: 60/046,200
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
; US-09-023-809B-3

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| Query Match | 100.00%; | Score | 2120; | DB | 3; | Length | 409; |
| Best Local Similarity | 100.0%; | Pred. No. | 1.9e-212; | | | | |
| Matches | 409; | Conservative | 0; | Mismatches | 0; | Indels | 0; |
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| DB | 1 | MSVFDKFNHGYVSEIGLETVLHVEPGREIDYITPARLDELFLFSAILSHDARKEHQS | 60 | | | | |
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| DB | 61 | FKVMKDRGINVVELTDLVAETVYDLASKAAKEEFIFTFLEETVPVLTANKKAVRAFLLS | 120 | | | | |
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| DB | 121 | KPTHEWVFPMGSIKYELGVSENELIVDPMNPLYFTRDPPASVGVNGVTIHFMRIVVRR | 180 | | | | |
| QY | 181 | RETLFARFVRNHPKLVKTPWYYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDTITLL | 240 | | | | |
| DB | 181 | RETLFARFVRNHPKLVKTPWYYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDTITLL | 240 | | | | |
| QY | 241 | AKNIKANKVEFKRIIVAINVPKWTNLMHLDLTMLDKKNKFLYSPIANDVFKFWDVLDVN | 300 | | | | |
| DB | 241 | AKNIKANKVEFKRIIVAINVPKWTNLMHLDLTMLDKKNKFLYSPIANDVFKFWDVLDVN | 300 | | | | |
| QY | 301 | GGAEPOPQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPLGV | 360 | | | | |
| DB | 301 | GGAEPOPQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPLGV | 360 | | | | |
| QY | 361 | IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMGMLSRKDKVKW | 409 | | | | |

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Db      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 2
US-09-564-559B-1
; Sequence 1, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-1

Query Match      100.0%; Score 2120; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.9e-212;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
Db      181 RETLFARFVRNHPKLVKTPWYDDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
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Qy      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 4
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; Sequence 2, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-2

Query Match      99.8%; Score 2116; DB 4; Length 409;
Best Local Similarity 99.8%; Pred. No. 4.9e-212;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      61 FVKIMKDRGINNVVELTDLVAETYDLASKAAKEEFITFLEETVPVLTANKKAVRAFLLS 120
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Db      121 KPTHEMVFEFMMSGITKYELGVSENELIVDPMNLYFTRDPPFASVGVNGVTIHFMRIVRR 180
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Db      301 GGAEPQPLNGPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
Qy      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db      361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 3
US-09-723-546-3
; Sequence 3, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14

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Db 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300
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Db 301 GGAEPQQLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360
QY 361 IGYDRNEKNTNAALKAAGITVLPFHGNQSLGMCNARCMSPLSRKDKVK 409
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RESULT 5
US-09-564-559B-3
; Sequence 3, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-3

Query Match 99.6%; Score 2112; DB 4; Length 409;
Best Local Similarity 99.8%; Pred. No. 1.3e-211;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 361 IGYDRNEKNTNAALKAAGITVLPFHGNQSLGMCNARCMSPLSRKDKVK 409

RESULT 6
US-09-564-559B-4
; Sequence 4, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-4

Query Match 99.4%; Score 2108; DB 4; Length 409;
Best Local Similarity 99.5%; Pred. No. 3.4e-211;
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MSVFDKFNIGHYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
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Db 61 FVKMKDRGINVVELTDLVAETVYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120
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Db 121 KPHEMVEFWMGSIKYELGVSENELIVDPMPNLVETROPFASVGNVGTIHFMRIVRR 180
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Db 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLVN 300
QY 301 GGAEPQQLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360
Db 301 GGAEPQQLNGLPLDKLLASIIKKEPVLIPIGGAGATEMEIARETNFDGNTYLAIKPGLV 360
QY 361 IGYDRNEKNTNAALKAAGITVLPFHGNQSLGMCNARCMSPLSRKDKVK 409
Db 361 IGYDRNEKNTNAALKAAGITVLPFHGNQSLGMCNARCMSPLSRKDKVK 409

RESULT 7
US-08-792-283A-8
; Sequence 8, Application US/08792283A
; Patent No. 5804183
; GENERAL INFORMATION:
; APPLICANT: Filpula, David
; APPLICANT: Wang, Maoliang
; TITLE OF INVENTION: Arginine Deiminase Derived From
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;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: ROBERTS & MERCANTI
;; STREET: 81 Tamarack Circle
;; CITY: Skillman
;; STATE: New Jersey
;; COUNTRY: United States
;; ZIP: 08558
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/792,283A
;; FILING DATE: 31-JAN-1997
;; CLASSIFICATION: 428
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mercanti, Michael N.
;; REGISTRATION NUMBER: 33966
;; REFERENCE/DOCKET NUMBER: 2131055
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-921-3500
;; TELEFAX: 609-921-9535
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 410 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mycoplasma hominis
;; STRAIN: PG21
;; CELL TYPE: unicellular
;;
US-08-792-283A-8

Query Match 99.0%; Score 2098.5; DB 1; Length 410;
Best Local Similarity 99.3%; Pred. No. 3.3e-210;
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGLETVLVHPEGRIDYITPARDELLEFSAILESHDARKEHQ 60
Db |||||

Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120
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Qy 121 -KPTHEVFMMSGITKYELGVSENELIVDPMPNLYFTRDPPFASVGVNGVTIHPMRYIVR 179
Db |||||

Qy 121 QKPTHEVFMMSGITKYELGVSENELIVDPMPNLYFTRDPPFASVGVNGVTIHPMRYIVR 180
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Qy 181 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDITL 240
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Qy 300 NGGAEPQVLNGLPLDKLLASIIINKEPVLPIGAGATEMIEIARETNFDGTNYLAIKPL 359
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Db |||||

US-09-105-908-8
;; Sequence 8, Application US/09105908
;; Patent No. 5916793
;; GENERAL INFORMATION:
;; APPLICANT: Filpula, David
;; APPLICANT: Wang, Maoliang
;; TITLE OF INVENTION: Arginine Deiminase Derived From
;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: ROBERTS & MERCANTI
;; STREET: 81 Tamarack Circle
;; CITY: Skillman
;; STATE: New Jersey
;; COUNTRY: United States
;; ZIP: 08558
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/105,908
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: US/08/792,283
;; APPLICATION NUMBER: US/08/792,283
;; FILING DATE: 31-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mercanti, Michael N.
;; REGISTRATION NUMBER: 33966
;; REFERENCE/DOCKET NUMBER: 2131055
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-921-3500
;; TELEFAX: 609-921-9535
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 410 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: No. 5916793 Relevant
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mycoplasma hominis
;; STRAIN: PG21
;; CELL TYPE: unicellular
;;
US-09-105-908-8

Query Match 99.0%; Score 2098.5; DB 2; Length 410;
Best Local Similarity 99.3%; Pred. No. 3.3e-210;
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGLETVLVHPEGRIDYITPARDELLEFSAILESHDARKEHQ 60
Db |||||

Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120
Db |||||

Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLS 120
Db |||||

Qy 121 -KPTHEVFMMSGITKYELGVSENELIVDPMPNLYFTRDPPFASVGVNGVTIHPMRYIVR 179
Db |||||

Qy 121 QKPTHEVFMMSGITKYELGVSENELIVDPMPNLYFTRDPPFASVGVNGVTIHPMRYIVR 180
Db |||||

Qy 180 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDITL 239
Db |||||

Qy 181 RRETLEFARFVRNHPKLVKTPWYDPAKMPLEGDVFIYNNETLVVGVSERTDITL 240
Db |||||

Qy 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLV 299
Db |||||

Qy 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLV 300
Db |||||

QY 300 NGGAEPPQVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPPVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIKPGL 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409
Db 361 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 410

RESULT 9

US-09-271-713-8
; Sequence 8, Application US/09271713
; Patent No. 6132713
; GENERAL INFORMATION:
; APPLICANT: Filpula, David
; APPLICANT: Wang, Maoliang
; TITLE OF INVENTION: Arginine Deiminase Derived From
; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTS & MERCANTI
; STREET: 81 Tamarack Circle
; CITY: Skillman
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08558
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,713
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,283
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mercanti, Michael N.
; REGISTRATION NUMBER: 33966
; REFERENCE/DOCKET NUMBER: 2131055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-921-3500
; TELEFAX: 609-921-9535
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 6132713 Relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycoplasma hominis
; STRAIN: PG21
; CELL TYPE: unicellular
US-09-271-713-8

Query Match 99.0%; Score 2098.5; DB 3; Length 410;
Best Local Similarity 99.3%; Pred. No. 3.3e-210;
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MSVFDKFGNIHYISEIGLETVLVHPEQREIDYITPARLDELLFSAILES HDARKEHQS 60
Db 1 MSVFDKFGNIHYISEIGLETVLVHPEQREIDYITPARLDELLFSAILES HDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPLTEANKKAVRAFLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPLTEANKKAVRAFLS 120
QY 121 -KPTHEMVFMMSGITKYELGVESENELIVDPMNLYFTRDPFPASVGVNGVTIHFMYRIVR 179

Db 121 QKPTHEMVFMMSGITKYELGVESENELIVDPMNLYFTRDPFPASVGVNGVTIHFMYRIVR 180
QY 180 RRETLFARFVFRNHPKLVKTPMYYPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVFRNHPKLVKTPMYYPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPPQVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPPVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIKPGL 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409
Db 361 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 410

RESULT 10

US-09-023-809B-2
; Sequence 2, Application US/09023809B
; Patent No. 6183738
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0028
; CURRENT APPLICATION NUMBER: US/09/023,809B
; CURRENT FILING DATE: 2000-02-13
; PRIOR APPLICATION NUMBER: 60/046,200
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-023-809B-2

Query Match 85.3%; Score 1807.5; DB 3; Length 410;
Best Local Similarity 84.4%; Pred. No. 8.1e-180;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDKFGNIHYISEIGLETVLVHPEQREIDYITPARLDELLFSAILES HDARKEHQS 60
Db 1 MSVFDKFGNIHYISEIGLETVLVHPEQREIDYITPARLDELLFSAILES HDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPLTEANKKAVRAFLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPLTEANKKAVRAFLS 120
QY 121 KPT-HEMVFMMSGITKYELGVESENELIVDPMNLYFTRDPFPASVGVNGVTIHFMYRIVR 179
Db 121 KPT-HEMVFMMSGITKYELGVESENELIVDPMNLYFTRDPFPASVGVNGVTIHFMYRIVR 180
QY 180 RRETLFARFVFRNHPKLVKTPMYYPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVFRNHPKLVKTPMYYPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPPQVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPPVINGLPDLKLLASIIINKEPVLIPIGGAGATEMEIARETNFGDTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409
Db 361 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 410

RESULT 11

Wed Nov 24 08:05:24 2004

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US-09-723-546-2
; Sequence 2, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-723-546-2
Query Match      85.3%; Score 1807.5; DB 4; Length 410;
Best Local Similarity 84.4%; Pred. No. 8.1e-180;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Db 61 FVAILKANDINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 13
US-09-564-559B-9
; Sequence 9, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-9
Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.1e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Db 61 FVAILKANDINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409
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; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-7
Query Match      84.6%; Score 1793.5; DB 4; Length 409;
Best Local Similarity 84.4%; Pred. No. 2.3e-178;
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Db 61 FVAILKANDINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 13
US-09-564-559B-9
; Sequence 9, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-9
Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.1e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDKNGIHVYSEIGELTVLVHPEGREIDYITPARLDELLFSAILESHDARKEHQS 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Db 61 FVAILKANDINVVELTDLVAETDYLASKAAKEEFIEETFLPETVPLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFFMMSGITKYELGVSENELIVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 179
Db 121 KKTSRKLVLMAGITKYDLGVEADHLLVDPMPNLVTRDPFASVGVNGVTIHFMRIVR 180
Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDLTLMDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIKPGL 359
Db 301 NGABEPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNPDGTNYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVK 409
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Db 121 KTSRKLVELMAGITKYDLGVEADHELIVDPNPNIYFTRDPFASVGNVTHFMRYKVR 180
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGVDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFSRFVRNHPKLVNTPWYDPAKMLSEGGDVFIYNNDTLVVGVSERTDLDITVL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPQPLNGPLDKLASIINKPVLPIPGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYAIRPGV 360
QY 360 VIGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKKAAGIKVLPFPHGNQLSLGMGNARCMPLSRKDVK 409

RESULT 14
US-09-564-559B-10
; Sequence 10, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOS0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-10

Query Match 84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.1e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKNGIHVYSIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDSEKNGIHVYSIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINNVETIDLVAEITYDLASQAKRKIEEFLEDSEPVLSAHEEVRNPLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVESNELIVDPMNPNIYFTRDPFASVGNVTHFMRYIVR 179
Db 121 KTSRKLVELMAGITKYDLGVEADHELIVDPNPNIYFTRDPFASVGNVTHFMRYKVR 180
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGVDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFSRFVRNHPKLVNTPWYDPAKMLSEGGDVFIYNNDTLVVGVSERTDLDITVL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPQPLNGPLDKLASIINKPVLPIPGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYAIRPGV 360
QY 360 VIGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMPLSRKDVK 408
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Search completed: November 23, 2004, 15:52:37
JOB time : 41 secs

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Db 361 VIGYSRNEKTNAAKKAAGIKVLPFPHGNQLSLGMGNARCMPLSRKDVK 409

RESULT 15
US-09-564-559B-8
; Sequence 8, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOS0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-8

Query Match 84.2%; Score 1785.5; DB 4; Length 409;
Best Local Similarity 83.9%; Pred. No. 1.6e-177;
Matches 343; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKNGIHVYSIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
Db 1 MSVFDSEKNGIHVYSIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVYDLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLS 120
Db 61 FVAILKANDINNVETIDLVAEITYDLASQAKRKIEEFLEDSEPVLSAHEEVRNPLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVESNELIVDPMNPNIYFTRDPFASVGNVTHFMRYIVR 179
Db 121 KTSRKLVELMAGITKYDLGVEADHELIVDPNPNIYFTRDPFASVGNVTHFMRYKVR 180
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGVDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETLFSRFVRNHPKLVNTPWYDPAKMLSEGGDVFIYNNDTLVVGVSERTDLDITVL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDVFKFWDYDLV 300
QY 300 NGGAEPQPLNGPLDKLASIINKPVLPIPGGAGATEMEIARETNFGDTNYLAIKPGL 359
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYAIRPGV 360
QY 360 VIGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKKAAGIKVLPFPHGNQLSLGMGNARCMPLSRKDVK 409
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2004, 15:34:09 ; Search time 157 Seconds
(without alignments)
934.524 Million cell updates/sec

Title: US-10-674-666-1
Perfect score: 2120
Sequence: 1 MSVFSKFNHIVHSEIGEL.....LGMGNARCMSPLSRDKVKW 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|---------------------|
| 1 | 2120 | 100.0 | 409 | 5 | AAE16134 | AAE16134 Mycoplasma |
| 2 | 2120 | 100.0 | 409 | 5 | ABG31996 | ABG31996 M. hominu |
| 3 | 2112 | 99.6 | 409 | 5 | AAE16136 | AAE16136 Mycoplasma |
| 4 | 2110 | 99.5 | 409 | 5 | AAE16135 | AAE16135 Mycoplasma |
| 5 | 2109 | 99.5 | 408 | 2 | AAW89442 | AAW89442 Mycoplasma |
| 6 | 2108 | 99.4 | 409 | 5 | AAE16137 | AAE16137 Mycoplasma |
| 7 | 1807.5 | 85.3 | 410 | 5 | ABG31995 | ABG31995 M. arthri |
| 8 | 1796.5 | 84.7 | 409 | 2 | AAW89441 | AAW89441 Mycoplasma |
| 9 | 1764.5 | 83.2 | 410 | 5 | ABG31994 | ABG31994 M. argini |
| 10 | 1763.5 | 83.2 | 410 | 5 | ABG76127 | ABG76127 Mycoplasma |
| 11 | 1753.5 | 82.7 | 409 | 2 | AAW89440 | AAW89440 Mycoplasma |
| 12 | 1733.5 | 81.8 | 409 | 2 | AAW24528 | AAW24528 Arginine |
| 13 | 1732.5 | 81.7 | 410 | 2 | AAW65454 | AAW65454 Arginine |
| 14 | 1632.5 | 77.0 | 405 | 2 | AAW05713 | AAW05713 Arginine |
| 15 | 1081.5 | 51.0 | 264 | 2 | AAW20500 | AAW20500 Cell grow |
| 16 | 1067.5 | 50.4 | 263 | 2 | AAW10854 | AAW10854 Arginine |
| 17 | 682.5 | 32.2 | 432 | 8 | ADM77935 | ADM77935 S. suis A |
| 18 | 681.5 | 32.1 | 413 | 5 | ABG32003 | ABG32003 B. lichen |
| 19 | 679 | 32.0 | 411 | 1 | AAW70278 | AAW70278 Streptoco |
| 20 | 679 | 32.0 | 411 | 5 | ABP26975 | ABP26975 Streptoco |
| 21 | 679 | 32.0 | 411 | 5 | ABG31997 | ABG31997 S. pyogen |
| 22 | 679 | 32.0 | 411 | 7 | ADC56694 | ADC56694 Streptoco |
| 23 | 678.5 | 32.0 | 410 | 5 | ABP26974 | ABP26974 Streptoco |
| 24 | 670.5 | 31.6 | 408 | 5 | ABG32004 | ABG32004 E. faecal |
| 25 | 667.5 | 31.5 | 417 | 7 | ADC96521 | ADC96521 E. faeciu |

| | | | | | | |
|----|-------|------|-----|---|----------|---------------------|
| 26 | 655 | 30.9 | 413 | 5 | ABG32002 | Abg32002 C. perfri |
| 27 | 652.5 | 30.8 | 409 | 8 | ADK47759 | Adk47759 Streptoco |
| 28 | 651.5 | 30.7 | 409 | 5 | ABG31998 | Abg31998 S. pneumo |
| 29 | 651.5 | 30.7 | 409 | 6 | ABU02572 | Abu02572 S. pneumo |
| 30 | 644.5 | 30.4 | 411 | 6 | ABW72707 | Abm72707 Staphyloc |
| 31 | 640.5 | 30.2 | 411 | 2 | AAW99068 | Aaw99068 Staphyloc |
| 32 | 640.5 | 30.2 | 422 | 5 | ABP38086 | Abp38086 Staphyloc |
| 33 | 640 | 30.2 | 408 | 6 | ADB10770 | Adb10770 Alloioococ |
| 34 | 640 | 30.2 | 417 | 5 | ADB10768 | Adb10768 Alloioococ |
| 35 | 632 | 29.8 | 410 | 5 | ABB49849 | Abb49849 Listeria |
| 36 | 631.5 | 29.8 | 410 | 5 | ABW55391 | Abw55391 Lactococ |
| 37 | 625 | 29.5 | 409 | 5 | ABG32005 | Abg32005 L. sake a |
| 38 | 618 | 29.2 | 420 | 5 | ABP39582 | Abp39582 Staphyloc |
| 39 | 612.5 | 28.9 | 410 | 5 | ABG31999 | Abg31999 B. burgdo |
| 40 | 604.5 | 28.5 | 394 | 4 | AAW81482 | Aaw81482 S. epider |
| 41 | 600.5 | 28.3 | 409 | 5 | ABG32000 | Abg32000 B. afzeli |
| 42 | 581.5 | 27.4 | 379 | 7 | ADH88142 | Adh88142 Enterococ |
| 43 | 519 | 24.5 | 406 | 4 | ABB52662 | Abb52662 Escherich |
| 44 | 476.5 | 22.5 | 415 | 4 | AAU58873 | Aau58873 Propionib |
| 45 | 476.5 | 22.5 | 415 | 6 | ABW55392 | Abw55392 Propionib |

ALIGNMENTS

RESULT 1

AAE16134
ID AAE16134 standard; protein; 409 AA.

XX AC AAE16134;

XX DT 26-MAR-2002 (first entry)

XX DE Mycoplasma hominis wild type arginine deiminase (ADI).

XX KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;
XX KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
XX KW septic shock; tumour.

XX OS Mycoplasma hominis.

XX PN WO200183774-A2.

XX PD 08-NOV-2001.

XX PP 02-MAY-2001; 2001WO-US014116.

XX PR 04-MAY-2000; 2000US-00564559.

XX PA (PHOB-) PHOENIX PHARMACOLOGICS INC.

XX PI Ensor CM, Holtsberg FW, Clark MA;

XX XX WPI; 2002-097497/13.

XX PT Modified arginine deiminase for improved manufacturing processes and for
XX PT treating cancer, is mutated to be free of a pegylation site at or
XX PT adjacent to its catalytic region.

XX PS Example 3; Fig 1; 34pp; English.

XX CC The invention relates to a modified arginine deiminase (ADI) for improved
XX CC manufacturing processes. The process comprises ADI modified to be free of
XX CC at least one pegylation site at or adjacent to its catalytic region. ADI
XX CC catalyses the conversion of arginine to citrulline and may be used to
XX CC eliminate arginine. ADI is useful for treating cancer, melanomas,
XX CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating
XX CC and inhibiting metastasis of tumour cells and other disease states. The
XX CC present sequence is Mycoplasma hominis wild type ADI

XX SQ Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;

```
Best Local Similarity 100.0%; Pred. No. 1.4e-193;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELLEFSAILESDDARKEHQ 60
DB 1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELLEFSAILESDDARKEHQ 60
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
DB 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
QY 121 KPTHEMVFEFMSGITKVELGVESENELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRR 180
DB 121 KPTHEMVFEFMSGITKVELGVESENELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDITILL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDITILL 240
QY 241 AKNIKANKEVEFKRIIVAINVPKWNTLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIIVAINVPKWNTLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300
QY 301 GGAEPOPQLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPOPQLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
DB 361 IGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 2
ABG31996
ID ABG31996 standard; protein; 409 AA.
AC ABG31996;
XX
XX
DT 06-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
XX
DE M. hominus arginine deiminase gene, HOMADIPRO.
XX
KW Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
KW autotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX
OS Mycoplasma hominis.
XX
XX WO200244360-A2.
XX
PD 06-JUN-2002.
XX
XX 19-SEP-2001; 2001WO-US029184.
XX
XX 28-NOV-2000; 2000US-00723546.
XX
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX
XX Clark MA;
XX
XX WPI; 2002-619003/66.
XX
XX Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
XX patient, comprises arginine deiminase covalently bonded by a linking
XX group such as succinimide to polyethylene glycol.
XX
XX Example 1; Fig 1; 59pp; English.
XX
XX The invention discloses a compound comprising arginine deiminase (ADI)
XX covalently bonded by a linking group to polyethylene glycol (PEG) having
XX a total weight average molecular weight of about 1000-50000. Also
XX disclosed is a method for enhancing the circulating half life or the
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CC tumoricidal activity of arginine deiminase by modifying the arginine
CC deiminase by covalently bonding the arginine deiminase by a linking group
CC to PEG. Normal cells can synthesize arginine from citrulline in a 2 step
CC process catalysed by argininosuccinate synthase and argininosuccinate
CC lyase. In contrast, many cancerous cells do not express argininosuccinate
CC synthase and are, therefore, autotrophic for arginine. Arginine deiminase
CC catalyses the conversion of arginine to citrulline and can be used to
CC eliminate arginine from the cancerous cells. The compound is useful for
CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC for treating and inhibiting metastases in a patient. When compared to
CC native arginine deiminase the compound retains most of its enzymatic
CC activity, and is far less antigenic, has a greatly extended circulating half-
CC life, and is much more efficacious in the treatment of tumours. The
CC sequence presented is the Mycoplasma hominus arginine deiminase gene,
CC HOMADIPRO. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 409 AA;
Query Match 100.0%; Score 2120; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.4e-193;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELLEFSAILESDDARKEHQ 60
DB 1 MSVPDSKFNHIVYSEIGELETVLVHPGREGIDYITPARDELLEFSAILESDDARKEHQ 60
QY 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
DB 61 FVKIMKDRGINVVELTDLVAETVDLASKAAKEFIETFLPETVPLTEANKKAVRAFLS 120
QY 121 KPTHEMVFEFMSGITKVELGVESENELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRR 180
DB 121 KPTHEMVFEFMSGITKVELGVESENELIVDPMPNLYFTRDPFASVGVNGVTIHFMRIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDITILL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERTDITILL 240
QY 241 AKNIKANKEVEFKRIIVAINVPKWNTLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIIVAINVPKWNTLMHLDTWLMDKNKFLYSPIANDVFKFWDYDLVN 300
QY 301 GGAEPOPQLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPOPQLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
DB 361 IGYDRNEKTNAAKKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 3
AAE16136
ID AAE16136 standard; protein; 409 AA.
XX
XX AAE16136;
XX
XX 26-MAR-2002 (first entry)
XX
XX Mycoplasma hominis modified arginine deiminase (ADI) #2.
XX
XX Arginine deiminase; ADI; cytosolic; antibacterial; immunosuppressive;
XX antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
XX septic shock; tumour; mutant; mutein.
XX
XX Mycoplasma hominis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 210 /note= "Wild type Pro substituted with Ser"
XX
XX WO200183774-A2.
```

```
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014116.
XX 04-MAY-2000; 2000US-00564559.
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX Ensor CM, Holsberg FW, Clark MA;
XX WPI; 2002-097497/13.
XX Modified arginine deiminase for improved manufacturing processes and for
PT treating cancer, is mutated to be free of a pegylation site at or
PT adjacent to its catalytic region.
XX Disclosure; Page 31-32; 34pp; English.
XX The invention relates to a modified arginine deiminase (ADI) for improved
CC manufacturing processes. The process comprises ADI modified to be free of
CC at least one pegylation site at or adjacent to its catalytic region. ADI
CC catalyses the conversion of arginine to citrulline and may be used to
CC eliminate arginine. ADI is useful for treating cancer, melanomas,
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating
CC and inhibiting metastasis of tumour cells and other disease states. The
CC present sequence is Mycoplasma hominis modified ADI protein
XX Sequence 409 AA;
XX Query Match 99.6%; Score 2112; DB 5; Length 409;
XX Best Local Similarity 99.8%; Pred. No. 8.1e-193;
XX Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSVFDKFNHIVYSGIETLVVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60
DB 1 MSVFDKFNHIVYSGIETLVVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFL 120
DB 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFL 120
QY 121 KPHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVNGVTIHPMRYIVRR 180
DB 121 KPHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVNGVTIHPMRYIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMQSIEGGDVFIYNNETLVVGVSERTDLDITLL 240
QY 241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
QY 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
DB 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
RESULT 4
AAE16135
ID AAE16135 standard; protein; 409 AA.
XX
AC AAE16135;
XX
DT 26-MAR-2002 (first entry)
XX
DE Mycoplasma hominis modified arginine deiminase (ADI) #1.
XX
```

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KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;
KW septic shock; tumour; mutant; mutain.
XX Mycoplasma hominis.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 111
FT Misc-difference /note= "Wild type Lys substituted with Pro"
FT Misc-difference 112 /note= "Wild type Lys substituted with Glu"
XX
XX WO200183774-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014116.
XX 04-MAY-2000; 2000US-00564559.
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX Ensor CM, Holsberg FW, Clark MA;
XX WPI; 2002-097497/13.
XX Modified arginine deiminase for improved manufacturing processes and for
PT treating cancer, is mutated to be free of a pegylation site at or
PT adjacent to its catalytic region.
XX Disclosure; Page 30-31; 34pp; English.
XX The invention relates to a modified arginine deiminase (ADI) for improved
CC manufacturing processes. The process comprises ADI modified to be free of
CC at least one pegylation site at or adjacent to its catalytic region. ADI
CC catalyses the conversion of arginine to citrulline and may be used to
CC eliminate arginine. ADI is useful for treating cancer, melanomas,
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating
CC and inhibiting metastasis of tumour cells and other disease states. The
CC present sequence is Mycoplasma hominis modified ADI protein
XX Sequence 409 AA;
XX Query Match 99.5%; Score 2110; DB 5; Length 409;
XX Best Local Similarity 99.5%; Pred. No. 1.3e-192;
XX Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSVFDKFNHIVYSGIETLVVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60
DB 1 MSVFDKFNHIVYSGIETLVVHEPGREIDYITPARLDELLFSAILES HDARKEHQ 60
QY 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFL 120
DB 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFEETVPVLTEANKKAVRAFL 120
QY 121 KPHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVNGVTIHPMRYIVRR 180
DB 121 KPHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVNGVTIHPMRYIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITLL 240
QY 241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLVN 300
QY 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPQQLNGPLDKLLASIIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
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Db 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFELEETVPLTEANKKAVRAFLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFELEETVPLTEANKKAVRAFLS 120
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 180
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 180
Qy 181 RETLFAFVFRNHPKLVKTPWYDPAWKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240
Db 181 RETLFAFVFRNHPKLVKTPWYDPAWKMSIEGGDVFIYNNETLVVGVSERTDLDITILL 240
Qy 241 ANNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPANDVFKFWDYDLVN 300
Db 241 ANNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPANDVFKFWDYDLVN 300
Qy 301 GGAEPOPQNLGLPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGNTNYLAIKPGLV 360
Db 301 GGAEPOPQNLGLPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGNTNYLAIKPGLV 360
Qy 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
Db 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409

RESULT 7
ABG31995
ID ABG31995 standard; protein; 410 AA.
XX
AC ABG31995;
XX
DT 15-NOV-2002 (first entry)
XX
DE M. arthritides arginine deiminase gene, ARTADIPRO.
XX
KW Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
KW autotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX
OS Mycoplasma arthritidis.
XX
PN WO200244360-A2.
PD
PF 06-JUN-2002.
PF 19-SEP-2001; 2001WO-US029184.
PR 28-NOV-2000; 2000US-00723546.
XX
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX
PI Clark MA;
XX
WPI; 2002-619003/66.
XX
PT Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
PT patient, comprises arginine deiminase covalently bonded by a linking
PT group such as succinimide to polyethylene glycol.
XX
PS Example 1; Fig 1; 59pp; English.
XX
CC The invention discloses a compound comprising arginine deiminase (ADI)
CC covalently bonded by a linking group to polyethylene glycol (PEG) having
CC a total weight average molecular weight of about 1000-50000. Also
CC disclosed is a method for enhancing the circulating half life or the
CC tumoricidal activity of arginine deiminase by modifying the arginine
CC deiminase by covalently bonding the arginine deiminase by a linking group
CC to PEG. Normal cells can synthesise arginine from citrulline in a 2 step
CC process catalysed by argininosuccinate synthase and argininosuccinate
CC lyase. In contrast, many cancerous cells do not express argininosuccinate

CC synthase and are, therefore, autotrophic for arginine. Arginine deiminase
CC catalyses the conversion of arginine to citrulline and can be used to
CC eliminate arginine from the cancerous cells. The compound is useful for
CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC for treating and inhibiting metastases in a patient. When compared to
CC native arginine deiminase the compound retains most of its enzymatic
CC activity, is far less antigenic, has a greatly extended circulating half-
CC life, and is much more efficacious in the treatment of tumours. The
CC sequence presented is the Mycoplasma arthritidis arginine deiminase gene,
CC ARTADIPRO
XX
SQ Sequence 410 AA;
Query Match 85.3%; Score 1807.5; DB 5; Length 410;
Best Local Similarity 84.4%; Pred. No. 1.1e-163;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;
Qy 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
Db 1 MSVFDKFGNIHYSEIGLETVLVHEPGREIDYITPARLDELLFSAILESHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFELEETVPLTEANKKAVRAFLS 120
Db 61 FVKIMKDRGINNVVELTDLVAETVDLASKAAKEFIETFELEETVPLTEANKKAVRAFLS 120
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 179
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 179
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 179
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRVIVR 179
Qy 181 RETLFAFVFRNHPKLVKTPWYDPAWKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 239
Db 181 RETLFAFVFRNHPKLVKTPWYDPAWKMSIEGGDVFIYNNETLVVGVSERTDLDITILL 240
Qy 240 ANNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPANDVFKFWDYDLVN 299
Db 240 ANNIKANKVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPANDVFKFWDYDLVN 299
Qy 241 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
Db 241 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVVK 409
RESULT 8
AAW89441
ID AAW89441 standard; protein; 409 AA.
XX
AC AAW89441;
XX
DT 18-MAR-1999 (first entry)
XX
DE Mycoplasma arthritidis arginine deiminase.
XX
KW Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritidis;
KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;
KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.
XX
OS Mycoplasma arthritidis.
XX
PN WO9851784-A1.
XX
PD 19-NOV-1998.
XX
PF 12-MAY-1996; 98WO-US009575.
XX
PR 12-MAY-1997; 97US-0046200P.
PR 13-FEB-1998; 98US-00023809.
XX
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX

PI Clark MA;
XX WPI; 1999-045227/04.
XX
XX New compound comprising arginine deiminase - covalently bonded via
PT linking group to polyethylene glycol, to enhance the half life of
PT arginine by this modification.
XX
XX Claim 6; Fig 1; 30pp; English.
XX
XX The present sequence represents Mycoplasma arthritis arginine
CC deiminase. The present invention describes: (1) a compound comprising
CC arginine deiminase (AD) covalently bonded via linking group to
CC polyethylene glycol (PEG), and having a molecular weight 12-40 kDa; and
CC (2) a composition as above, but where the linking group is selected from
CC a malimide group, an amide group, an imide group, a carbamate group, an
CC ester group, an epoxy group, a carboxyl group, a hydroxyl group, a
CC carbohydrate, a tyrosine group, a cysteine group and/or a histidine
CC group. AD can be used in the treatment of tumours, e.g. melanomas,
CC hepatomas and sarcomas, and to inhibit metastasis. The modified AD has an
CC enhanced circulating half life
XX
SQ Sequence 409 AA;

Query Match 84.7%; Score 1796.5; DB 2; Length 409;
Best Local Similarity 84.4%; Pred. No. 1.2e-162; Mismatches 34; Indels 1; Gaps 1;
Matches 345; Conservative 29;

QY 1 MSVPDSKFGIHVYSEIGELETVLVHPEPGREIDYITPARDELFFSAILSHDARKEHQS 60
DB 1 MSVPDSKFGIHVYSEIGELESVLVHPEPGREIDYITPARDELFFSAILSHDARKEHQS 60

QY 61 FVKIMKDRGINNVVELTDLVAETYLASAKAEFEIETFPVLTTEANKKAVRAFLLS 120
DB 61 FVAILKANDINNVVELTDLVAETYLASAKAEFEIETFPVLTTEANKKAVRAFLLS 120

QY 121 KPT-HEMVEPMMSGITKYELGVSENELIVDPMNLYFTDRDPFASVGVNGVTIHFMYIVR 179
DB 121 KTSRKLVEIMMAGITKYDLGIEADHELIVDPMNLYFTDRDPFASVGVNGVTIHFMYIVR 180

QY 180 RRETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 239
DB 181 RRETLFSRFVRNHPKLVNTFWYDDPAMKLSIEGDDVFIYNNETLVVGVSERTDLDITL 240

QY 240 LAKNIKANKEVEFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 299
DB 241 LAKNLVANKCEFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPQPOLNGLPLDKLASIINKPEVLIPIGGAGATEMEIARETNPDGNTYLAIRPGV 359
DB 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGNTYLAIRPGV 360

QY 360 VIGYDRNEKNTNAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDKVK 408
DB 361 VIGYSRNEKNTNAALKAAGIKVLPFHGNQSLGNGNARCMSPLSRKDKVK 409

RESULT 9
ABG31994
ID ABG31994 standard; protein; 410 AA.
XX
AC ABG31994;
XX
XX 15-NOV-2002 (first entry)
XX
XX M. arginini arginine deiminase gene, ADIPROT.
XX
XX Arginine deiminase; cytotstatic; ADI; polyethylene glycol; PEG; arginine;
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX
OS Mycoplasma arginini.
XX

PN WO200244360-A2.
XX
XX 06-JUN-2002.
XX
XX 19-SEP-2001; 2001WO-US029184.
XX
XX 28-NOV-2000; 2000US-00723546.
XX
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX
XX Clark MA;
XX
XX WPI; 2002-619003/66.
XX
XX Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
PT patient, comprises arginine deiminase covalently bonded by a linking
PT group such as succinimide to polyethylene glycol.
XX
XX Example 1; Fig 1; 59pp; English.
XX
XX The invention discloses a compound comprising arginine deiminase (ADI)
CC covalently bonded by a linking group to polyethylene glycol (PEG) having
CC a total weight average molecular weight of about 1000-50000. Also
CC disclosed is a method for enhancing the circulating half life or the
CC tumoricidal activity of arginine deiminase by modifying the arginine
CC deiminase by covalently bonding the arginine deiminase by a linking group
CC to PEG. Normal cells can synthesize arginine from citrulline in a 2 step
CC process catalysed by argininosuccinate synthase and argininosuccinate
CC lyase. In contrast, many cancerous cells do not express argininosuccinate
CC synthase and are, therefore, auxotrophic for arginine. Arginine deiminase
CC catalyses the conversion of arginine to citrulline and can be used to
CC eliminate arginine from the cancerous cells. The compound is useful for
CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC for treating and inhibiting metastases in a patient. When compared to
CC native arginine deiminase the compound retains most of its enzymatic
CC activity, is far less antigenic, has a greatly extended circulating half-
CC life, and is much more efficacious in the treatment of tumours. The
CC sequence presented is the Mycoplasma arginini arginine deiminase gene,
CC ADIPROT
XX
SQ Sequence 410 AA;

Query Match 83.2%; Score 1764.5; DB 5; Length 410;
Best Local Similarity 82.0%; Pred. No. 1.4e-159;
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVPDSKFGIHVYSEIGELETVLVHPEPGREIDYITPARDELFFSAILSHDARKEHQS 60
DB 1 MSVPDSKFGIHVYSEIGELESVLVHPEPGREIDYITPARDELFFSAILSHDARKEHQS 60

QY 61 FVKIMKDRGINNVVELTDLVAETYLASAKAEFEIETFPVLTTEANKKAVRAFLLS 120
DB 61 FVAILKANDINNVVELTDLVAETYLASAKAEFEIETFPVLTTEANKKAVRAFLLS 120

QY 121 KPT-HEMVEPMMSGITKYELGVSENELIVDPMNLYFTDRDPFASVGVNGVTIHFMYIVR 179
DB 121 KTSRKLVEIMMAGITKYDLGIEADHELIVDPMNLYFTDRDPFASVGVNGVTIHFMYIVR 180

QY 180 RRETLFARFVRNHPKLVKTPWYDDPAMKPIEGGDVFIYNNETLVVGVSERTDLDITL 239
DB 181 RRETLFSRFVRNHPKLVNTFWYDDPAMKLSIEGDDVFIYNNETLVVGVSERTDLDITL 240

QY 240 LAKNIKANKEVEFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 299
DB 241 LAKNLVANKCEFKRIIVAINVVKWTNLMHLDITLMDKKNKFLYSPIANDVFKFWDYDLV 300

QY 300 NGGAEPQPOLNGLPLDKLASIINKPEVLIPIGGAGATEMEIARETNPDGNTYLAIRPGV 359
DB 301 NGGAEPQPVENGLPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGNTYLAIRPGV 360

QY 360 VIGYDRNEKNTNAALKAAGITVLPFHGNQSLGNGNARCMSPLSRKDKVK 409
DB 361 VIGYSRNEKNTNAALKAAGIKVLPFHGNQSLGNGNARCMSPLSRKDKVK 410

RESULT 10

ABB76127

ID ABB76127 standard; protein; 410 AA.

AC ABB76127;

XX XX

DT 15-JUL-2002 (first entry)

XX XX

Mycoplasma arginini recombinant arginine deiminase.

DE Arginine deiminase; enzyme; angiogenesis; inhibitor; cytostatic;
KW antiarthritic; ophthalmological; antipsoriatic; dermatological;
KW anticseborrheic; antidiabetic.
XX OS
OS Mycoplasma arginini.
XX WO200209741-A1.
XX 07-FEB-2002.
XX 27-JUL-2001; 2001WO-KR001281.
XX 27-JUL-2000; 2000KR-00043454.
XX (ANGI-) ANGIOLAB INC.
PA Min BH, Park MO, Kim MY, Park BY, Chun BG, Kang SW, Moon CH;
PI WPI; 2002-392400/41.
DR N-PSDB; ABU56974.
XX XX
XX Composition for inhibiting angiogenesis in the treatment of e.g.
PT arthritis, cancer, psoriasis comprises arginine deiminase as an active
PT ingredient.
XX PS Disclosure; Page 42-44; 46pp; English.
XX XX
XX The present sequence is that of the arginine deiminase of Mycoplasma
CC arginini ATCC 23243. The enzyme was overexpressed in Escherichia coli
CC using a coding sequence (see ABUS56974) modified to reflect codon usage in
CC E. coli, in particular the replacement of 5 in-frame TGA codons
CC (recognised as Trp in mycoplasma) by TGG codons. The invention relates to
CC the use of arginine deiminase as an angiogenesis inhibitor. A claimed
CC pharmaceutical composition for inhibiting angiogenesis comprises arginine
CC deiminase, including the present recombinant enzyme, as an active
CC ingredient, preferably conjugated to an activated polymer. The
CC composition is used to treat or inhibit a disease selected from angina,
CC angiodysplasia, arthritis, diabetic retinopathy, premature infant's
CC retinopathy, neovascular glaucoma, corneal disease, involutional macula,
CC macular degeneration, pterygium, retinal degeneration, retrolental
CC fibroplasia, granular conjunctivitis, psoriasis telangiectasia, pyogenic
CC granuloma, seborrhoeic dermatitis, acne, cancer and metastasis (all
XX claimed)
XX SQ Sequence 410 AA;

Query Match 83.2%; Score 1763.5; DB 5; Length 410;
Best Local Similarity 82.0%; Pred. No. 1.7e-159;
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVFDKFNHGVSEIGLETVLVHEPQREIDYTTPARLDLFSATLESHDARKKHQS 60
Db 1 MSVFDKFNHGVSEIGLESVLVHEPQREIDYTTPARLDLFSATLESHDARKKHQ 60

QY 61 FVKIMKRGDINVELTDLVAETDYDLSAKAAKEEFTEFLETVPVLTEANKAVRAFLS 120
Db 61 FVAELKANDINVVELIDLVAETYDLSAQEADKLIEFELEDSEPLSEEKVVRNFLKA 120

QY 121 KPT-HEMVFMSGTYKYBELGVESNELIVDPMPNLYFTROPFPASVGNGVTIHPRVIYR 179
Db 121 KXTSRELVEIMMAGITTKDLGLEAEOHELIVDPMPNLYFTROPFPASVGNGVTIHYMYKKR 180

Db 1 MSVDSKFGIHYVSEIGLESLVHEPGREIDYITPARDELLEFSAILESDDARKEHQ 60
QY 61 FVKIMKDRGINVVELTDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
Db 61 FVAELKANDINVVELIDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
QY 121 KPT-HEMVPMGSIKYELGVSENELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYR 179
Db 121 KTSRLVIMMAGITKYDLGIEADHELIVDPNLYFTRDPPASVGVNGVTIHFMYIYR 180
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERDLDITLL 239
Db 181 QRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERDLDITLL 240
QY 240 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKDKFLYSPANDVFKFWDYDLV 299
Db 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKDKFLYSPANDVFKFWDYDLV 300
QY 300 NGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGL 359
Db 301 NGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIRPGV 360
QY 360 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409

RESULT 12
AAR24528 standard; protein; 409 AA.
XX AC AAR24528;
XX AC AAR24528;
DT 25-NOV-1992 (first entry)
DE Arginine deiminase.
XX AD; PEG.
XX Mycoplasma arginini.
XX JP04121187-A.
PD 22-APR-1992.
PF 10-SEP-1990; 90JP-00239387.
PR 10-SEP-1990; 90JP-00239387.
XX (NIHA) NIPPON MINING CO.
XX WPI; 1992-188063/23.
DR N-PSDB; AAQ25395.
PT Polyethylene glycol modified arginine deaminase prepn. - by covalently
PT bonding arginine deiminase and ethylene glycol, useful as anticancer
PT drug.
XX Disclosure; Fig 1; 16pp; Japanese.
PS The sequence given is arginine deiminase (AD) which, within the scope of
CC the invention is modified by polyethylene glycol (PEG). This modification
CC is caused by covalently bonding AD with PEG or its derivatives. This
CC modified compound has equal anticancer effect to AD, but the blood
CC stability is raised and the antigenicity is reduced. This product has
CC low toxicity
XX Sequence 409 AA;
XX Query Match 81.8%; Score 1733.5; DB 2; Length 409;
XX Best Local Similarity 80.7%; Pred. No. 1.3e-156;
XX Matches 330; Conservative 40; Mismatches 38; Indels 1; Gaps 1;

QY 2 SVFDSKFGIHYVSEIGLESLVHEPGREIDYITPARDELLEFSAILESDDARKEHQSF 61
Db 1 SVFDSKFGIHYVSEIGLESLVHEPGREIDYITPARDELLEFSAILESDDARKEHQSF 60
QY 62 VKIMKDRGINVVELTDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLSK 121
Db 61 FVAELKANDINVVELIDLVAETDYLAKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLSK 120
QY 122 PT-HEMVPMGSIKYELGVSENELIVDMPNLYFTRDPPASVGVNGVTIHFMYIYR 180
Db 121 KTSRLVIMMAGITKYDLGIEADHELIVDPNLYFTRDPPASVGVNGVTIHFMYIYR 180
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERDLDITLL 240
Db 181 QRETLFARFVRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVGVVSERDLDITLL 240
QY 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKDKFLYSPANDVFKFWDYDLV 300
Db 241 LAKNIKANKEVEFKRIVAINVVKWTNLMHLDTWLMDKDKFLYSPANDVFKFWDYDLV 300
QY 301 NGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIKPGLV 360
Db 301 NGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGTNYLAIRPGV 360
QY 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409
Db 361 VIGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVK 409
RESULT 13
AAR65454
ID AAR65454 standard; protein; 410 AA.
XX AC AAR65454;
XX AC AAR65454;
DT 19-NOV-1998 (first entry)
DE Arginine deiminase (ADI) amino acid sequence.
XX Arginine, ADI; recombinant; tumour; cancer; nitric oxide;
XX nitric oxide synthase.
XX Mycoplasma arthritis.
XX WO9833519-A1.
PD 06-AUG-1998.
PF 27-JAN-1998; 98WO-US001635.
PR 31-JAN-1997; 97US-00792283.
XX (ENZO-) ENZON INC.
XX Filpula DR, Wang M;
XX WPI; 1998-437174/37.
DR N-PSDB; AAV07550.
XX Nucleic acid encoding arginine deiminase of Mycoplasma arthritis -
XX useful for, e.g. treating tumours, cancers and nitric oxide-related
XX conditions.
PS Claim 1; Page 33-34; 54pp; English.
XX This present sequence produces an arginine deiminase protein (ADI), an
CC enzyme that hydrolyses arginine. To obtain the ADI nucleic acid, the M.
CC arthritis strain 14152 was isolated from the American type culture
CC collection, where from the arginine deiminase gene could be identified by
CC the use of standard techniques. The protein encoded by this gene can be
CC produced recombinantly as well as naturally to treat ADI-susceptible
CC conditions, particularly tumours and cancers, or nitric oxide-related

CC conditions that require modulation of nitric oxide synthase. It can also
modulate the adverse effects of a low protein diet

XX Sequence 410 AA;

Query Match 81.7%; Score 1732.5; DB 2; Length 410;
Best Local Similarity 80.5%; Pred. No. 1.6e-156;
Matches 330; Conservative 36; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHGVSEIGELTVLVEHPGKEIDYITPARDELLEFSAILESHDARKEHQS 60
Db 1 MSVDSKFNHGVSEIGELTVLVEHPGKEIDYITPARDELLEFSAILESHDARKEHKE 60
Qy 61 FVKIMKDRGINNVVELTDLVAETVYDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS 120
Db 61 FVAELKKGGINNVVELVDLIIVETVYDLASKAAKEELLEEFLDSDVPVLSDEHRAVKKFLOS 120
Qy 121 -KPTHEVMVFMMGKITKYELGVSENELIVDPMNLYFTTRDPPFASVGVNGVTIHFMYRIVR 179
Db 121 QKSTRSLVETMIAGITKHLKIESDLELIIVDPMNLYFTTRDPPFASVGVNGVTIHFMYRIVR 180
Qy 180 RRETLPARFVRNHPKLVKTPWYDDPAKMPLEGDDVFIYNNETLVVGVSERTDLDITIL 239
Db 181 QRETLPARFVRNHPKLVNTPWYDDPAEGLTIEGGDVFIYNNETLVVGVSERTDLDITIL 240
Qy 240 LAKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV 299
Db 241 LAKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV 300
Qy 300 NGGAEPQPLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGNTNLAIKPGL 359
Db 301 NGGDAPQVNDGLPLEDLKLSIIKKPTLPIAGAGASQIDIERETHFDGNTNLAIVAPGI 360
Qy 360 VIGYDRNEKNTNAALKAAGITVLPFHGNQLSLGGMGNARCMSPLSRKDVKW 409
Db 361 VIGYARNEKNTNAALKAAGITVLPFRGNQLSLGGMGNARCMSPLSRKDVKW 410

RESULT 14
AAR05713
ID AAR05713 standard; protein; 405 AA.
XX AC AAR05713;
XX AC AAR05713;
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 16-AUG-1990 (first entry)
XX DE Arginine deaminase.
XX DE Arginine deaminase; carcinostatic; cancer; ds.
XX OS Unidentified.
XX PN JP02053490-A.
XX PD 22-FEB-1990.
XX PF 16-AUG-1988; 88JP-00202759.
XX PR 16-AUG-1988; 88JP-00202759.
XX PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX DR WPI; 1990-103119/14.
XX DR N-PSDB; AAQ03739.
XX PT Arginine de:iminase gene - where DNA contains base sequence that codes
PT aminoacid sequence of arginine de:iminase composing polypeptide.
XX PS Disclosure; Fig 1; 18pp; Japanese.
XX XX Expression vector transformed by the gene may be used to produce large

CC quantities of arginine deaminase, useful as a carcinostatic. (Updated on
10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
PA field.)

XX Sequence 405 AA;

Query Match 77.0%; Score 1632.5; DB 2; Length 405;
Best Local Similarity 78.0%; Pred. No. 5.7e-147;
Matches 319; Conservative 44; Mismatches 41; Indels 5; Gaps 5;

Qy 2 SVFDSKFNHGVSEIGELTVLVEHPGKEIDYITPARDELLEFSAILESHDARKEHQS 61
Db 1 SVFDSKFNHGVSEIGELTVLVEHPGKEIDYITPARDELLEFSAILESDARKEHKE 60
Qy 62 VKIMKDRGINNVVELTDLVAETVYDLASKAAKEEFIEFTLEETVPVLTEANKKAVRAFLLS- 120
Db 61 VELKKGGINNVVELVDLIIVETVYDLASKAAKEELLEEFLDSDVPVLSPEQKAKVEFLKSL 120
Qy 121 KPTHEVMVFMMGKITKYELGVSENELIVDPMNLYFTTRDPPFASVGVNGVTIHFMYRIVR 180
Db 121 KSTKELIQYMMGKITKYDLGIKADKELIVDPMKLYFTTRDPPFASVGVNGVTIHFMYRIVR 180
Qy 181 RETLPARFVRNHPKLVKTPWYDDPAKMPLEGDDVFIYNNETLVVGVSERTDLDITIL 240
Db 181 RETLFSKFTFNHPKLVKTP-YYDPAMKLSIEGDDVFIYNNETLVVGVSERTDLDITIL 239
Qy 241 AKNIKANKKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV 300
Db 240 AKNIKANKKEVEFKRIIVAINVPK--TNLMHLDT--UTMLDKNKFLYSPIANDVFKF--DYDLV 296
Qy 301 GGAEPOPQPLNGPLDKLLASIIKKEPVLPIGGAGATEMEIARETNFDGNTNLAIKPGLV 360
Db 297 GGSNPEPVVNGPLDKLLESIIKKPVLPIAGKGAETEIVAVETHFDGNTNLAIKEGVV 356
Qy 361 IGYDRNEKNTNAALKAAGITVLPFHGNQLSLGGMGNARCMSPLSRKDVKW 409
Db 357 VGYSRVNKTNAALKAANGIKVLPFGNQLSLGGMGNARCMSPLSRKDVKW 405

RESULT 15
AAR20500
ID AAR20500 standard; protein; 264 AA.
XX AC AAR20500;
XX AC AAR20500;
DT 25-MAR-2003 (revised)
DT 24-APR-1992 (first entry)
XX DE Cell growth inhibiting peptide.
XX DE Cancer.
XX KW Mycoplasma arginini.
XX OS
XX FH Key Location/Qualifiers
FT Peptide 1..8 /label= N-terminal peptide
FT Peptide 31..38 /label= tryptic
FT Peptide /notes= "B"
FT Peptide 60..65 /label= tryptic
FT Peptide /notes= "C"
FT Peptide 138..145 /label= tryptic
FT Peptide /notes= "F"
FT Peptide 161..164 /label= tryptic
FT Peptide /notes= "E"
FT Peptide 189..195 /label= tryptic
FT Peptide /notes= "A"
FT Peptide 197..209

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FT /label= tryptic
FT /note= "D"
FT 294..300
FT /label= tryptic
FT /note= "G"
XX
XX JF03284699-A..
XX
XX 16-DEC-1991.
XX
XX 12-APR-1990; 90JP-00097265.
XX
XX 09-FEB-1990; 90JP-00029975.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
XX (HAYB ) HAYASHIBARA BIOCHEMICAL LAB.
XX
XX WPI; 1992-037730/05.
XX N-PSDB; AAQ20239.
XX
XX Protein obtd. from mycoplasma arginine, inhibiting cell growth - used as
XX immunosuppressant in organ transplant, as allergy suppressant and
XX treating auto-immune disease and malignant tumours.
XX
XX Claim 1; Fig 4; 20pp; Japanese.
XX
XX The protein is a novel growth inhibitor and can be used for various
XX treatments involving the suppression of cell growth. Tryptic peptide "B"
XX was used to design probes (see AAQ22582, 82 and 84) for the cloning of
XX the gene encoding the protein (see AAQ20239). (Updated on 25-MAR-2003 to
XX correct PA field.)
XX
XX SQ Sequence 264 AA;
Query Match 51.0%; Score 1081.5; DB 2; Length 264;
Best Local Similarity 78.8%; Pred. No. 1.4e-94;
Matches 208; Conservative 28; Mismatches 27; Indels 1; Gaps 1;
Qy 1 MSVFDSKFNCHVYSEIGELETVLVHEPFGREIDYITPARLDELFSAILSHDARKEHQ 60
Db 1 MSVFDSKFNCHVYSEIGELETVLVHEPFGREIDYITPARLDELFSAILSHDARKEHQ 60
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEETFPVLTANKKAVRAFLS 120
Db 61 FVAELKANDINVVELIDLVAETDYLASQEAQKLIIEFLEDESEFVLSSEHKVVRNFLKA 120
Qy 121 KPT-HEMVEFMMSGITKYLGVSENELIVDPMNLYFTRDPPFASVNGVGTIHFMYIVR 179
Db 121 KTSRKLVEIMMAGITTKYDLGIEADHELIVDPMNLYFTRDPPFASVNGVGTIHFMYIKVR 180
Qy 180 RRETLFARFVRNHPKLVKTPMYVDPAKMDIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 QRETLFGRFVRNHPKLVKTPMYVDPAKMDIEGGDVFIYNNETLVVGVSERTDLDITL 240
Qy 240 LAKNIKANKEVEFKRIVAINVPKW 263
Db 241 LAKNIVANKECEFKRIVAINVPKW 264
```

Search completed: November 23, 2004, 15:47:50
Job time : 161 secs

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OM protein - protein search, using sw model

Run on: November 23, 2004, 15:34:27 ; Search time 192 Seconds
(without alignments)
1225.668 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVDFSKFNGIHVYSIGEL.....LGMGNARCMPLSRKDKVKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2115 | 99.8 | 408 | 1 | ARCA MYCHO |
| 2 | 1763.5 | 83.2 | 409 | 1 | ARCA MYCAR |
| 3 | 1721.5 | 81.2 | 409 | 2 | Q9RND4 |
| 4 | 1169.5 | 55.2 | 452 | 2 | Q8EVP6 |
| 5 | 1103 | 52.0 | 408 | 2 | Q7NBF0 |
| 6 | 1057 | 49.9 | 404 | 1 | ARCA MYCPN |
| 7 | 986 | 46.5 | 409 | 2 | Q6KI67 |
| 8 | 986 | 46.5 | 409 | 2 | AAT27709 |
| 9 | 708.5 | 33.4 | 410 | 2 | Q6HP29 |
| 10 | 707.5 | 33.4 | 410 | 2 | Q81111 |
| 11 | 705.5 | 33.3 | 410 | 2 | Q73B87 |
| 12 | 705.5 | 33.3 | 410 | 2 | AAS39407 |
| 13 | 688 | 32.5 | 403 | 2 | Q8KZ88 |
| 14 | 682.5 | 32.2 | 409 | 2 | Q8GG81 |
| 15 | 681.5 | 32.1 | 413 | 1 | ARCA BACLI |
| 16 | 679 | 32.0 | 410 | 1 | ARCA_STRPY |
| 17 | 678.5 | 32.0 | 410 | 2 | Q8DWQ2 |
| 18 | 678.5 | 32.0 | 410 | 2 | Q8E2K0 |
| 19 | 677 | 31.9 | 410 | 1 | ARCA STRP3 |
| 20 | 672 | 31.7 | 411 | 2 | Q6TK74 |
| 21 | 672 | 31.7 | 411 | 2 | AAR30322 |
| 22 | 670.5 | 31.6 | 408 | 2 | Q93K67 |
| 23 | 660 | 31.1 | 413 | 1 | ARCA CLOPE |
| 24 | 655.5 | 30.9 | 409 | 2 | Q9KJG1 |
| 25 | 651.5 | 30.7 | 409 | 1 | ARCA STRPN |
| 26 | 650 | 30.7 | 410 | 2 | Q8GND5 |
| 27 | 648.5 | 30.6 | 411 | 2 | Q6GG7 |
| 28 | 644.5 | 30.4 | 411 | 1 | ARCA_STAAN |
| 29 | 644.5 | 30.4 | 411 | 2 | Q7AS72 |
| 30 | 644.5 | 30.4 | 411 | 2 | Q6GG39 |
| 31 | 644.5 | 30.4 | 411 | 2 | CAD98181 |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 32 | 641.5 | 30.3 | 411 | 1 | ARCI_STAEP | O8CG95 staphylococ |
| 33 | 640.5 | 30.2 | 411 | 1 | ARCA_STAAM | Q99R02 staphylococ |
| 34 | 638.5 | 30.1 | 410 | 1 | ARCA_LACLC | Q9K576 lactococcus |
| 35 | 638.5 | 30.1 | 410 | 2 | Q9KGV5 | Q9KGV5 lactococcus |
| 36 | 638 | 30.1 | 408 | 1 | ARCA_LISIN | Q92F77 listeria in |
| 37 | 632 | 29.8 | 410 | 1 | ARCA_LISMO | Q8YAS0 listeria mo |
| 38 | 631.5 | 29.8 | 410 | 1 | ARCA_LACLA | P58013 lactococcus |
| 39 | 631 | 29.8 | 410 | 2 | Q725C1 | Q725C1 listeria mo |
| 40 | 631 | 29.8 | 410 | 2 | AAT02840 | Aat02840 listeria |
| 41 | 625 | 29.5 | 409 | 1 | ARCA_LACSK | O53088 lactobacill |
| 42 | 624.5 | 29.5 | 410 | 2 | Q73QJ2 | Q73QJ2 treponena d |
| 43 | 624.5 | 29.5 | 410 | 2 | AAS10946 | Aas10946 treponema |
| 44 | 624.5 | 29.5 | 468 | 2 | Q8RDD8 | Q8RDD8 thermoanaer |
| 45 | 617.5 | 29.1 | 415 | 2 | Q8VW56 | Q8VW56 oenococcus |

ALIGNMENTS

RESULT 1

| | | | | |
|----|---|-----------|------|---------|
| ID | ARCA_MYCHO | STANDARD; | PRT; | 408 AA. |
| AC | P41141; | | | |
| DT | 01-FEB-1995 (Rel. 31, Created) | | | |
| DT | 01-FEB-1995 (Rel. 31, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD). | | | |
| GN | Names-arca; | | | |
| OS | Mycoplasma hominis. | | | |
| OC | Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. | | | |
| OX | NCBI_TaxID=2098; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=92396053; PubMed=1522817; | | | |
| RA | Harasawa R., Koshimizu K., Kitagawa M., Asada K., Kato I.; | | | |
| RT | "Nucleotide sequence of the arginine deiminase gene of Mycoplasma hominis." | | | |
| RL | Microbiol. Immunol. 36:661-665(1992). | | | |
| CC | -1- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3). | | | |
| CC | -1- PATHWAY: Arginine degradation via arginine deiminase; first step. | | | |
| CC | -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential). | | | |
| CC | -1- SIMILARITY: Belongs to the arginine deiminase family. | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| DR | EMBL, D13314; BAA02571.1; -- | | | |
| DR | HAWAP; MF_00242; --; 1. | | | |
| DR | InterPro; IPR003198; Amidino trans. | | | |
| DR | InterPro; IPR003876; Arg deiminase. | | | |
| DR | Pfam; PF02274; Amidinotransf; 1. | | | |
| DR | PRINTS; PR01466; ARGDEIMINASE. | | | |
| DR | TIGRFAMs; TIGR01078; arca; 1. | | | |
| KW | Arginine metabolism; Hydrolase. | | | |
| FT | ACT_SITE 396 396 | | | |
| FT | INACT_SITE 0 | | | |
| FT | By similarity. | | | |
| FT | Amidino-cysteine intermediate (By similarity). | | | |
| FT | ACT_SITE 396 396 | | | |
| FT | INACT_SITE 0 | | | |
| FT | By similarity. | | | |
| FT | Amidino-cysteine intermediate (By similarity). | | | |
| SQ | SEQUENCE 408 AA; 46182 MW; 53A11D637DBBE93 CRC64; | | | |
| | Query Match 99.8%; Score 2115; DB 1; Length 408; | | | |
| | Best Local Similarity 100.0%; Pred. No. 4.2e-136; | | | |
| | Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |

QY 2 SVFDSKFNHVSSEIGELTVLHPGREGIDYITPARDELLEFSAILESHDARKEHQSF 61

DB 1 SVFDSKFNHVSSEIGELTVLHPGREGIDYITPARDELLEFSAILESHDARKEHQSF 60

QY 62 VKIMKDRGINVVELTDLVAETVDLASKAAKEEPIETFLEETVPVLTANKAVRAFLSK 121


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RX MEDLINE=20353471; PubMed=10894746;
RA Dybvig K., French C.T., Voelker L.L.;
RT "Construction and use of derivatives of transposon Tn4001 that
function in Mycoplasma pulmonis and Mycoplasma arthritis.";
RL J. Bacteriol. 182:4343-4347(2000).
DR EMBL; AF182646; AAD54448.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
SQ SEQUENCE 409 AA; 46039 MW; 7PEDC7F182BFF5C7 CRC64;

Query Match 81.2%; Score 1721.5; DB 2; Length 409;
Best Local Similarity 80.4%; Pred. No. 3.1e-109;
Matches 329; Conservative 38; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MSVDSKFNFGHIVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILSHDARKEHQS 60
Db 1 MSVDSKFKGHIVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILSHDARKEHE 60

Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFLBETVPVLTEANKAVRAFLS 120
Db 61 FVAELKKRGINVVELDLIVETDYLASKAAKEKLEEFLLDSDAPVLSDEHRAAVKFLQS 120

Qy 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTTRDPFASVNGVGTIHFMRIVR 179
Db 121 QKSTRSLVSEYMIAGITKHDLDKESDLEIVDPMPNLYFTTRDPFASVNGVGTIHFMRIVR 180

Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 QRETLPFRFVSNHPKLVNTPWYDPAEGLSIEGDVFIYNNETLVVGVSERTDLDITL 240

Qy 240 LAKNIKANKEVEFKRIVAINVVKWNLMLHDLTMTLDKMKFLYSPDIANDVFKFWYDVL 299
Db 241 LAKNIKANKEVEFKRIVAINVVKWNLMLHDLTMTLDKMKFLYSPDIANDVFKFWYDVL 300

Qy 300 NGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFDGNTYLAIKPGL 359
Db 301 NGGDAPOFVNGPLDPLDKLASIIGKPTLPIAGAGASQIDIERETHFDGNTYLAIPGI 360

Qy 360 VIGYDRNEKTNAAKAGITVLPHGNQLSLGNGNARCMSPLSRKDVK 408
Db 361 VIGYARNEKTNAAKAGITVLPHGNQLSLGNGNARCMSPLSRKDVK 409

RESULT 4
Q8EVF6 PRELIMINARY; PRT; 452 AA.
AC Q8EVF6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Arginine deiminase.
GN OrderedLocusNames=MYP86080;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004172; BAC44398.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.

us-10-674-666-1.rup

DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR Complete proteome.
SQ SEQUENCE 452 AA; 51045 MW; B25CCD15165E59F4 CRC64;

Query Match 55.2%; Score 1169.5; DB 2; Length 452;
Best Local Similarity 56.4%; Pred. No. 1.6e-71;
Matches 237; Conservative 68; Mismatches 92; Indels 23; Gaps 4;

Qy 1 MSVFD--SKFNGHIVYSEIGELETVLVHPGREGIDYITPARLDELLFSAILSHDARKEH 58
Db 43 MSSIDKNSLNGINIVYSEIGELKEVLVHTPGDIRYAPSRLEELLFSAYLKADTAIEEH 102

Qy 59 OSFVKIMKDRGINVVELTDLVAETDYLASKAAKEEFIEFLBETVPVLTEANKAVRAFL 118
Db 103 KGFVKILQNGIKVIQCDLVASTYELCKEVRNSFIEQYLDALPVLKKEIRPVVVDYL 162

Qy 119 LSKPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTTRDPFASVNGVGTIHFMRIV 178
Db 163 LSPPTVQVVRKMSGILANELNIKQDNPLIIDGMPNLYFTTRDPFASVNGVGTIHFMRIV 222

Qy 179 RRETLPARFVRNHPKLVKTPWYD-PAKMPPIEGGDVFIYNNETLVVGVSERTDLDIT 237
Db 223 RKREVFISRFVFTNPKYKNTPRYFDIVGNNGTIEGGDIFVYNSKTLVIGNSERTNFAAI 282

Qy 238 TLLAKNIKANKEVEFKRIVAINVVKWNLMLHDLTMTLDKMKFLYSPDIANDVFKFWYD 297
Db 283 ESVAKNIQANKOCTFRIVIVNPPMPNMLHDLTMTLDYDKFLYSPNNMNVLLKWEID 342

Qy 298 LVNGGAEPQPLNGPLDKLASIINKEPVLPIPGAGATEMEIARETNFD 348
Db 343 -----LVNPKVFKVEKGTLEEVLYSIIDKKPLIPIAGKANGLDIETHFD 391

Qy 349 GTNYLAIKPGLVIGYDRNEKTNAAKAGITVLPHGNQLSLGNGNARCMSPLSRKDVK 408
Db 392 GTNYLTIAFGVGVYERNEKTKALVEAGIKVLFSNGSQLSLGMSARCMSPLEIRENLK 451

RESULT 5
Q7NBF0 PRELIMINARY; PRT; 408 AA.
AC Q7NBF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arca (EC 3.5.3.6).
GN Name=arca; OrderedLocusNames=MYCGA3290; ORFNames=MGA_1220;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=22830409; PubMed=12949158;
RA Papazisi L., Gorton T.S., Kutieh G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).
DR EMBL; AE016968; AAP56679.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR Complete proteome; Hydrolase.
SQ SEQUENCE 408 AA; 47084 MW; 36EC0BF5A6A8F58A CRC64;

Query Match 52.0%; Score 1103; DB 2; Length 408;
Best Local Similarity 52.2%; Pred. No. 4.9e-67;
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RESULT 6
ARCA_MYCPN
ID ARCA_MYCPN STANDARD; PRT; 404 RA.
AC 75475; P75474;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).
GN
DN
GE
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / MI29;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelsreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C., Herrmann R.;
RA "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RL Nucleic Acids Res. 24:4420-4449 (1996).
[2]
RN
RP CONCEPTUAL TRANSLATION.
RA
RA Bairoch A.;
RL Unpublished observations (SEP-2000).
CC -1- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -1- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the arginine deiminase family.
CC -1- CAUTION: This is a conceptual translation; potential frameshifts were corrected to restore a more likely protein sequence.
-----
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CC
CC EMBL; AF0000052; AAB96180.1; ALT FRAME.
DR

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| | | | | | | |
|--|---|--|--------------------|------------|-------------|--|
| Query Match | | 46.5%; | Score 986; | DB 2; | Length 409; | |
| Best Local Similarity | | 48.4%; | Pred. No. 4.8e-59; | | | |
| Matches 198; | | Conservative 73; | Mismatches 120; | Indels 18; | Gaps 7; | |
| QY | 11 | IHVSEIGELTVLVHPEGREIDYITPARDELLEFSAILESHPDARKEHQSFKVIMKDRGI | 70 | | | |
| Db | 8 | INVSEIGELKKVLIHTPGNELKYVSPYRLDELLFSNVLEWREAKEHNEFIQKLKSEGV | 67 | | | |
| QY | 71 | NVVELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAFL--SKPTHEMVE | 128 | | | |
| Db | 68 | EPVELTDLVAESPEESIKVKNDFIRQYLDPEATPILDGLTKQKLFPFFLDIKHSTRKTIE | 127 | | | |
| QY | 129 | FMSGITKVELGVES--ENELIVDPMPNLYFTTRDPFASVGVNGVTIHFMRVYVRRRETLFAR | 187 | | | |
| Db | 128 | LWMSGITQKDISISHERELIIDPMNLYFSRDNFISGNSVLIISNMKYKTRKEITFTD | 187 | | | |
| QY | 188 | FVFRNHPKLVKTPWYDDP-----MKMPIEGGDVFIYNNETLVVGVVSERTDLDITITLAKN | 243 | | | |
| Db | 188 | FIPKHNPLYKKNMAFERKDLNNOISIEGGDVLVYSKEILIGISERTITMSAILELAEN | 247 | | | |
| QY | 244 | IKANKEVEFKRIIVAINVPKWTNLMHLDTWLMDKNKELYSPANDVFKFW-----DYDLV | 299 | | | |
| Db | 248 | FKTKRK-SFKKIYGVVEVPKWNLMHLDTWLMDYDKFIYSPNVLTDLKFWENLNDYEKI | 306 | | | |
| QY | 300 | NGGABPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDCGTNYLAIKPGL | 359 | | | |
| Db | 307 | S-----SKELHA-SLSEFLKLIIGKDPILIPIGKGASQITIDIEINFVAANYLVIRPGV | 360 | | | |
| QY | 360 | VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGNGNARCMSPLSRKDVK | 408 | | | |
| Db | 361 | VIGYSRNYETQKALEGHGVKVIAPFEGNQLSLGNGSSRCMSMPLIRSNLK | 409 | | | |
| RESULT 9 | | | | | | |
| Q6HP29 | | | | | | |
| ID | Q6HP29 | PRELIMINARY; | PRT; | 410 AA. | | |
| AC | G6HP29; | | | | | |
| DT | 05-JUL-2004 | (TREMELrel. 27, Created) | | | | |
| DT | 05-JUL-2004 | (TREMELrel. 27, Last sequence update) | | | | |
| DT | 05-JUL-2004 | (TREMELrel. 27, Last annotation update) | | | | |
| DE | Arginine deiminase (EC 3.5.3.6). | | | | | |
| GN | Name=arCA; ORFNames=BT9727_0341; | | | | | |
| OS | Bacillus thuringiensis serovar konkukian str. 97-27. | | | | | |
| OC | Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; | | | | | |
| OC | Bacillus thuringiensis serovar konkukian. | | | | | |
| OX | NCBI_TaxID=281309; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN=97-27; | | | | | |
| RA | Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., | | | | | |
| RA | Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., | | | | | |
| RA | Richardson P., Rubin E., Tice H.; | | | | | |
| RL | Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. | | | | | |
| DR | EMBL; AB017355; AAT58997.1; -. | | | | | |
| DR | InterPro; IPR003198; Amidino trans. | | | | | |
| DR | InterPro; IPR003876; Arg deiminase. | | | | | |
| DR | Pfam; PF02274; Amidinotransf; 1. | | | | | |
| DR | PRINTS; PR01466; ARGDEIMINASE. | | | | | |
| DR | TIGRFAMs; TIGR01078; arCA; 1. | | | | | |
| KW | Hydrolase. | | | | | |
| SQ | SEQUENCE 410 AA; 46922 MW; E1FE4927484E42BD CRC64; | | | | | |
| Query Match 33.4%; Score 708.5; DB 2; Length 410; | | | | | | |
| Best Local Similarity 40.2%; Pred. No. 4.2e-40; | | | | | | |
| Matches 166; Conservative 74; Mismatches 150; Indels 23; Gaps 9; | | | | | | |
| QY | 11 | IHVSEIGELTVLVHPEGREIDYITPARDELLEFSAILESHPDARKEHQSFKVIMKDRGI | 70 | | | |
| Db | 5 | IHVTSEIGELQVLLKRPKEVENTPQYLOQLLFDIDIPYLIQKEHDFAGTLANRGV | 64 | | | |
| QY | 71 | NVVELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAFLSKPTHEMVEFM | 130 | | | |
| Db | 65 | EVLYLEKLAEEA--LVDKKLEEFVDRIILKEQADVVAH--QTLKEYLLSFSNEELIQKI | 121 | | | |
| QY | 131 | MSGITK-----YELGVESNELIVDPMPNLYFTTRDPFASVGVNGVTIHFMRVYV | 179 | | | |
| Db | 122 | MGGVRAKNETSKTHLYEL-MEDHYPPYLDPMNPYFTTRDPAASVGDGLTINKREPAR | 180 | | | |
| Query Match 46.5%; Score 986; DB 2; Length 409; | | | | | | |
| Best Local Similarity 48.4%; Pred. No. 4.8e-59; | | | | | | |
| Matches 198; Conservative 73; Mismatches 120; Indels 18; Gaps 7; | | | | | | |
| QY | 11 | IHVSEIGELTVLVHPEGREIDYITPARDELLEFSAILESHPDARKEHQSFKVIMKDRGI | 70 | | | |

| | | | |
|----|-------------------------------|--|-----|
| | : :: : ::: : : | 241 ERLAKNL-FSRQNKIKKVLAIETPKRAFMEHLDVTFTVMDVDYDKFTHIPALQGPKGNMNYI | 299 |
| Db | | | |
| | : :: : ::: : : | 297 DLVNGGAEPPQL-NGLPDLKLASIIIN-KEPVLPIGGAGATEWEIARETNFGCTNYLA | 354 |
| Qy | | | |
| | : :: : ::: : : | 300 ILEKGSDEETLKITHRTSLMEALKEVLGLSELVLPCGGGDV--IASAREQWDSNTLYA | 357 |
| Db | | | |
| | : :: : ::: : : | 355 IKPLGVITYDRNEKTNAALKAAGTITVPFHFNQLSLGMGNARCMSMPISRKDV | 407 |
| Qy | | | |
| | : :: : ::: : : | 358 IAPGWVTDYNNYSNLTLLREHGTEVLSELSRSGRGGRCMGPVTRKDI | 410 |
| Db | | | |

RESULT 11
Q73E87
ID Q73E87
PRELIMINARY;
PRT: 410 AA.

05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=arcA; OrderedLocuNames=BCE0472;
OS *Bacillus cereus* (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
NCBI_TaxID=222523;
[1]
RN SEQUENCE FROM N.A.
RP PubMed=14960714;
RX
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to *Bacillus anthracis* pX01.";
RL *Nucleic Acids Res.* 32:977-988(2004).
DR EMBL; AE017265; AAC39407.1; -.
DR TIGR; BC50472; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf. 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TrIRFAMS; TIGR01078; arca; 1.
DR Complete proteome; Hydrolase.
SQ Complete 410 AA; 46938 MW; 8D7846C8D206579A CRC64;
KW SEQUENCE

| | | | |
|----|----|--|-----|
| DB | 5 | IHTVSEIGELQTVLLKPKGKVENLTPDYLOQLLFFDDIPYLPITIQKEHDYFAQTLNRGV | 64 |
| QY | 71 | NVVELTDLVAETVYDLASKAAKEEFIEFLEETVPVLTPEANKKAVRAFLILSKPTHEMVEFM | 130 |

65 EVLYERLAAEA--LVDKLREEFVDRIKKGQADNVVAH-QTLKEYLLSFSNEELQKI 121
DB
QV 131 MSGITK-----YELGVSESENEILVDPMPNI.VETRDPA SVGNGVTHIEMPVIVP 178

Db 122 MGGVRKNEIETSKKTHLYEL-MEDHYFFYLDPMNLYFTRDPAASVGDGTLINKMREPAR 180

| | | | |
|----|-----|--|-----|
| Qy | 180 | RRETLFARFVRNHPKLVK--TPWYYDPAKMPPIEGDDVFIYNNETLVVGVSERTLDITI | 237 |
| Dh | 181 | PPSEIEMVETKVDDPFEEFNVPDITAPDQVKEITGGDEETIIEETITATGVSAFNSAVAT | 240 |

Qy 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVFKEFWDY 296

Db 241 ERLAKNL-FSRQNKIKKVLAI EIPKCRAPMHLDTVTFTMVDYDKFTIHPALIQPKGNMNIY 299

Db 300 ILEKGSDEETLKTHRTSLMEALKEVLGSELVLPCGGDV--IASAREOWNDGSNTLA 357

